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(54) Title: IMMUNOLOGICAL CONJUGATES OF OMPC AND HIV-SPECIFIC SELECTED PRINCIPAL NEUTRALIZATION EPITOPES

(57) Abstract

Immunological conjugates of HIV-specific selected principal neutralization epitopes are prepared. These epitopes bind a broadly neutralizing human monoclonal antibody specific for the HIV principal neutralization epitope(s) and are identified from oligopeptide epitope libraries. The conjugates are useful for vaccination against AIDS or ARC, as well as in the production of other HIV-specific broadly neutralizing antibodies for passive immunity against AIDS or ARC.

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FI	Finland				

TITLE OF THE INVENTION

IMMUNOLOGICAL CONJUGATES OF OMPC AND HIV-SPECIFIC SELECTED PRINCIPAL NEUTRALIZATION EPITOPES

BACKGROUND OF THE INVENTION

This application is related to U.S. 07/684,090, filed April 12, 1991, which is a continuation-in-part of U.S. 07/538,451, filed June 15, 1990, which applications are assigned to MedImmune, a Merck licensor. This application is also related to Merck cases 18709, 17858, 17943, 17944, 17945, 18114, 18154, and 18155.

Acquired Immune Deficiency Syndrome (AIDS) is the clinical manifestation of the apparent infection of CD4 helper T-cells and other cell targets by human immunodeficiency virus (HIV), also previously referred to as human T-lymphotropic virus type III (HTLV-III), Lymphoadenopathy-associated virus (LAV), or AIDS-related virus (ARV) (hereinafter collectively "HIV"). AIDS is a transmissible deficiency of cellular immunity characterized by opportunistic infections and certain malignancies. A similar disease, AIDS-related complex (ARC), shares many of the epidemiological features and immune abnormalities with AIDS, and often precedes the clinical manifestations of AIDS.

AIDS is a disease of a virus with a unique collection of attributes. HIV itself targets the immune system; it possesses a reverse transcriptase capable of turning out highly mutated progeny; it is sequestered from the immune system and it has a hypervariable sequence in the (env) region. See, e.g., Hilleman, M.R., Vaccine 6, 175 (1988); Barnes, D.M., Science 240, 719 (1988).

One consequence of these attributes is the diversity of HIV serotypes. The principal neutralizing determinant is an epitope residing in a hypervariable region of the (env) region. As a result, neutralizing antibodies directed against this epitope are generally extremely type-specific; that is, they neutralize only the parental virus and not

other variants. Appropriate immunological therapies for AIDS require special consideration of this serological diversity. In particular, it is widely believed that a likely AIDS vaccine will be polyvalent and comprise HIV determinants corresponding to each serotype.

Neutralization is now regarded as one of the key features in the successful design of an HIV immunological therapy. When a virus-specific antibody neutralizes its virus, it blocks continued replication of the virus, but the precise mechanism is not fully characterized and is thought to vary with virus and target cell. See, e.g, Dimmock, N.J., Trends in Biochem. Sci. 12, 70 (1987).

Applicants have now formulated and reduced to practice a unique method to make vaccines suitable for the serological diversity of HIV and the requirements of neutralization. Applicants employ monoclonal antibodies to define a broadly neutralizing response, then identify oligopeptide epitopes bound by these monoclonal antibodies out of a large random or semi random array or library. The identified epitopes do not have to share any protein sequence with the native HIV protein used to generate the monoclonal antibodies in the first place.

Recently, a broadly neutralizing monoclonal antibody against HIV has been discovered. This "447 antibody" binds to about 90% of all known HIV serotypes and neutralizes HIV. It was isolated from a human patient.

Applicants have used the 447 antibody to screen phage libraries of synthetic random or semi random oligopeptides. Applicants have discovered novel homologous oligopeptides useful as neutralization epitopes specific for HIV, known hereafter as selected principal neutralization epitopes (SPNEs). These oligopeptides are of synthetic origin.

Applicants have conjugated the oligopeptides of interest to an immunological carrier to provide an immunological conjugate useful as an AIDS vaccine. Alternatively, this immunological conjugate(s) is useful for generating better and improved broadly neutralizing antibodies for HIV, which are in turn useful for passive immunization and like therapies. The SPNEs as well as their immunological conjugates are also useful as reagents in the assay of virus in a human host, and in screening blood in blood banks.

A method for screening phage epitope libraries with an antibody of desired specificity or screening antibody is also described. For this screening, applicants have developed a novel selection procedure for the selection of phages bearing epitopes that bind antibody of desired specificity. The screening method of the present invention includes such selection, and, optionally, an identification method for identifying phages bearing desired epitopes.

BRIEF DESCRIPTION OF THE INVENTION

Synthetic amino acid sequences of Table A that bind a broadly neutralizing human monoclonal antibody (447 antibody) specific for the

HIV principal neutralization determinant are selected and identified from oligopeptide epitope libraries, and are useful in immunological conjugates with OMPC for vaccination against AIDS or ARC, as well as in the production of other HIV-specific broadly neutralizing antibodies for passive immunity against AIDS or ARC. Screening methods for selecting and/or identifying desired oligopeptide epitopes from phage epitope libraries are also described. The SPNES and their conjugates are also useful in the detection of HIV, or antibodies to HIV in blood samples, for the purpose of screening, clinical evaluation and diagnosis.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows the consensus peptide 58 and variants thereof, derived from isolated peptides from the Alpha Library. Thus the consensus peptide has an N-terminal sequence beginning Trp Asp Gly..., or, as variants, Trp Tyr Gly... or Trp Tyr Ala... or Trp Asp Ala...

Figure 2 illustrates one embodiment of the method of screening phage epitope libraries. Selection and identification are included.

ABBREVIATIONS AND DEFINITIONS

AIDS	Acquired immune deficiency syndrome
ARC	AIDS-related complex
conjugation	The process of covalently attaching 2 (sometimes 3) molecules each containing one or more immunological determinants, e.g., HIV envelope fragments and OMPC
conjugate	Result of conjugation, also known as an antigenic conjugate or immunological conjugate. Coconjugates are a special subgenus of conjugates.
GXG	Gly-Xaa-Gly, wherein Xaa is any amino acid.
GPXR	Gly-Pro-Xaa-Arg, wherein Xaa in this sequence is any amino acid except Gly. SEQ. ID NO:146.
HIV	Generic term for the presumed etiological agent of AIDS and/or ARC, also referred to as strains HTLV-III, LAV, and ARV

Library	A collection of DNA or oligopeptide sequences, of defined length, with or without limited sequence restrictions
OMPC	Outer membrane proteosome
PCR	Polymerase chain reaction
poly (gly, ser, ala, val)	a linear, random polymer of amino acids selected from the group consisting of glycine, serine, alanine or valine.
Recombinant fusion polypeptide (RFP)	A polypeptide or oligopeptide expressed as a contiguous translation product from a spliced foreign DNA in a recombinant eukaryotic or procaryotic expression system, wherein the spliced foreign DNA is derived from 2 or more coding sequences of different origin, and joined together by ligation or PCR.
Recombinant protein	A polypeptide or oligopeptide expressed by foreign DNA in a recombinant eukaryotic or procaryotic expression system.
Recombinant expression system	A cell containing a foreign DNA expressing a foreign protein or a foreign oligopeptide.

SPNE Selected Principal Neutralization Epitope, which is a principal neutralization determinant bound by one or more broadly neutralizing antibodies. SPNE is defined as including consensus sequences. SPNE may have one or two flexible flanking region(s) of poly (gly, ser, ala, val) of 1-10 amino acids in length.

Amino Acids

Full Name	Three-letter symbol	One-Letter symbol
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Asn or Asp	Asx	B
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Gln or Glu	Glx	Z
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T

Amino Acids cont'd.

Full Name	Three-letter symbol	One-Letter symbol
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V
Norlencine	Nle	

Nucleotides Bases in DNA or RNA

Name	One-letter symbol
Adenine	A
Cytosine	C
Guanine	G
Thymine	T
Uracil	U

The terms "protein," "peptide," "oligopeptide," and "polypeptide" and their plurals have been used interchangeably to refer to chemical compounds having amino acid sequences of five or more amino acids. "Amino acid" refers to any of the 20 common amino acids for which codons are naturally available, and are listed in the table of amino acids given above.

When any variable (e.g. SPNE) occurs more than one time in any constituent or in Formula I, its definition on each occurrence is independent of its definition at every other occurrence. Also, combinations of substituents and/or variables are permissible only if such combinations result in stable compounds.

SPNE oligopeptides may exist as peptides, as internal sequences in e.g. phage pIII proteins, in immunological conjugates with outermembrane proteosome, or as a fragment of a fusion protein with an immunoenhancer sequence such as Hepatitis B core. The position of SPNE in a fusion protein may be N-terminal, internal or C-terminal.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides HIV selected principal neutralization epitopes of synthetic origin, immunological conjugates of these epitopes with a carrier such as OMPC, and methods of treating or preventing AIDS or ARC with these conjugates. Also described is a method of screening these epitopes from phage epitope libraries.

The epitopes of the present invention bind an HIV broadly neutralizing antibody and were originally identified in the screening of phage epitope libraries having randomly or semi randomly generated epitope polypeptides accessible to the antibody. These screened polypeptides are hereinafter the selected principal neutralization epitope (SPNE) polypeptides. The sequences of these polypeptides were deduced from their corresponding DNA sequence, determined by the polymerase chain reaction. The SPNE polypeptides including consensus sequences thereof are characterized as having the sequences of Table A.

TABLE A

SEQ ID NO:2:

Trp	Arg	Leu	Gly	Pro	Gly	Arg	Gly	Ser	Met	Pro	Cys	Arg	Leu	Gly
1				5					10					15

SEQ ID NO:3:

Gln Gly Leu Leu Arg Val Leu Tyr Ala Phe Gly Pro Gly Arg Val
1 5 10 15

SEQ ID NO:6:

His Ser Gln Ala Val Lys Phe Gly Pro Gly Arg Thr Leu Val Pro
1 5 10 15

SEQ ID NO:8:

Asp Leu Gln Ala Arg Ser Lys Thr Tyr Phe Tyr Gly Pro Gly Arg
1 5 10 15

SEQ ID NO:13:

Leu Leu Leu Ile Gly Pro Gly Arg Glu Leu Arg Pro Ile Asn Leu
1 5 10 15

SEQ ID NO:15:

Phe Phe Tyr Gly Pro Gly Arg Tyr Pro Pro Arg Phe Lys Leu Gly
1 5 10 15

SEQ ID NO:18:

Cys Ala Thr Ser Ile Gly Gly Val Leu Phe Gly Pro Gly Arg Gly
1 5 10 15

SEQ ID NO:19:

Trp Arg Met Met Leu Gly Pro Gly Arg Asp Tyr Ala Gly Pro Ala
1 5 10 15

SEQ ID NO:21:

Arg Ile Arg Leu Pro Arg Gly Pro Gly Arg Pro Gln Thr Thr Met
1 5 10 15

SEQ ID NO:23:

Leu Leu Arg Thr Ile Met Ile Gly Pro Gly Arg Leu Leu His Ser
1 5 10 15

SEQ ID NO:25:

Gly Gln Ile Ile Phe Ile Gly Pro Gly Arg Leu Gly Asn Gly Glu
1 5 10 15

SEQ ID NO:26:

Leu Gln Leu Leu Ile Gly Pro Gly Arg Thr Val Gly Lys Ile Arg
1 5 10 15

SEQ ID NO:28:

Thr Lys Ile Gly Pro Gly Arg Val Phe Asp Gly Arg Trp Arg Phe
1 5 10 15

SEQ ID NO:30:

Ile Leu Phe Gly Pro Gly Arg Cys Ser Val Asp Ala Val Ser Gly
1 5 10 15

SEQ ID NO:31:

Tyr Leu Ala Met Arg Gly Ala Gly Tyr Met Ile Gly Pro Ala Arg
1 5 10 15

SEQ ID NO:32:

Asn Cys Ser Val His Val Gly Ala Gly Arg Asn Ser Ala Trp Cys
1 5 10 15

SEQ ID NO:33:

Asn Arg Tyr Gly Pro Gly Arg Val Gly Phe Val Arg Ser Gln Pro
1 5 10 15

SEQ ID NO:34:

Ala Arg Gly Trp Gly Gly Val Phe Tyr Gly Pro Gly Arg Gly Glu
1 5 10 15

SEQ ID NO:35:

Tyr Gly Arg Phe Ser Phe Gly Pro Gly Arg Gly Tyr Met Val Ile
1 5 10 15

SEQ ID NO:36:

Tyr Tyr Tyr Arg Asn Val Leu Val Gly Pro Gly Arg Trp Trp Leu
1 5 10 15

SEQ ID NO:38:

Arg Phe Gln Glu Gly Gln Lys Val Leu Val Gly Pro Gly Arg Arg
1 5 10 15

SEQ ID NO:39:

Ser Cys Met Thr Ser Val Leu Val Gly Pro Gly Arg Gln Asp Asn
1 5 10 15

SEQ ID NO:40:

Gly Ile Leu Arg Gln Pro Leu Leu Ile Gly Pro Gly Arg Ala Pro
1 5 10 15

SEQ ID NO:41:

Trp Asp Thr Leu Gly Trp Val Val Ser Asn Phe Gly Pro Gly Arg
1 5 10 15

SEQ ID NO:43:

Gln Ile Trp Tyr Phe Gly Pro Gly Arg Ser Gln Ser Gly Ser Met
1 5 10 15

SEQ ID NO:47:

Pro Tyr Ser Asp Leu Leu Leu Ser Lys Tyr Phe Gly Pro Gly Arg
1 5 10 15

SEQ ID NO:48:

Leu Asp Gln Tyr Arg Val Leu Leu Trp Gly Pro Gly Arg Thr Thr
1 5 10 15

SEQ ID NO:49:

Val Leu Lys Ile Leu Arg His Ala Tyr Phe Gly Pro Gly Arg Trp
1 5 10 15

SEQ ID NO:50:

Val Arg His Met Gly Pro Gly Arg Gly Met Val Leu Gly Ile Thr
1 5 10 15

SEQ ID NO:51:

Asn Tyr Phe Gly Pro Gly Arg Gly Gly Val Val Val Thr Gly His
1 5 10 15

SEQ ID NO:52:

Gln Val Phe Gly Pro Gly Arg Thr Asn Pro Arg Ser Asn Leu Leu
1 5 10 15

SEQ ID NO:55:

Phe Asp Gly Gln Ser Lys Val Val Leu Arg Gly Pro Gly Arg Gly
1 5 10 15

SEQ ID NO:58:

Trp Asp Gly Leu Gly Trp Gln Ile Val His Phe Gly Pro Gly Arg Gly
1 5 10 15

Gly Asn Gly Ile Asn Leu Gly Ala
20

SEQ ID NO:61:

Gly Ala Gly His Val Gly Pro Gly Arg Tyr Gly Ala Leu Ser
1 5 10

SEQ ID NO:63:

Ser Thr Arg His Leu Gly Pro Gly Arg Val Glu Gly Val Leu
1 5 10

SEQ ID NO:64:

Gly Val His Arg Phe Gly Pro Gly Arg Gly Glu Gly Met Val
1 5 10

SEQ ID NO:65:

Gly Gly Tyr His Trp Gly Pro Gly Arg Gly Ser Val Glu Ala
1 5 10

SEQ ID NO:66:

Gln Ala Trp His Phe Gly Pro Gly Arg Asp His Gly Glu
1 5 10

SEQ ID NO:67:

Lys Ala Asn His Tyr Gly Pro Ser Arg Gly Pro Gly Ser Arg
1 5 10

SEQ ID NO:68:

Leu Leu Gly Pro Gly Arg Gly Ser Ser Ser Val Arg Gly Glu Leu
1 5 10 15

SEQ ID NO:69:

Ser Gly Trp Trp Gly Gly Val His Val Gly Pro Gly Arg Gly Thr
1 5 10 15

SEQ ID NO:70:

Trp Ser Lys Arg Glu Ser Val Met Phe Gly Pro Gly Arg Gly Thr
1 5 10 15

SEQ ID NO:71:

Trp Asp Ser Arg Ala Thr Leu Arg Leu Gly Pro Gly Arg Ser Ser
1 5 10 15

SEQ ID NO:72:

Gly Lys Val Phe Tyr Gly Pro Gly Arg Glu Trp His Ala
1 5 10

SEQ ID NO:73:

Ala Arg Val Phe Leu Gly Pro Gly Arg Gly Val Val Tyr Asp
1 5 10

SEQ ID NO:74:

Arg Val Gln Lys Leu Gly Pro Gly Arg Gln Thr Ala Ser Gly
1 5 10

SEQ ID NO:75:

Lys Leu Gly Pro Gly Arg Gly Gly Tyr Phe Gly Ala Gln Val
1 5 10

SEQ ID NO:76:

Arg Lys Val Asn Ile Gly Pro Gly Arg Val His Gly Asn Ser
1 5 10

SEQ ID NO:77:

Arg Gly Val Lys Ile Gly Pro Gly Arg Ile Ala Ser Gly Tyr
1 5 10

SEQ ID NO:78:

Lys Asp Leu His Ile Gly Pro Gly Arg Met Asp Gly Leu Arg
1 5 10

SEQ ID NO:79:

Ala Gln Arg Ser His Leu Ile Gly Pro Gly Arg Ala Glu Thr Gly
1 5 10 15

SEQ ID NO:81:

Arg Gln Val Met Leu Gly Pro Gly Arg Gly Asp Arg Leu Glu
1 5 10

SEQ ID NO:83:

Lys Phe Val Glu Leu Gly Pro Gly Arg Lys Gly Gln Gly
1 5 10

SEQ ID NO:84:

Asp Arg Gly Ser Arg Phe Val Leu Leu Gly Pro Gly Arg Met Gly
1 5 10 15

SEQ ID NO:85:

Glu Gln Leu His Arg Leu Val Ala Phe Gly Pro Gly Arg Ala Ala
1 5 10 15

SEQ ID NO:86:

Leu Pro Ser Val Asn Leu Gly Pro Gly Arg Asn Ala Arg Lys Gly
1 5 10 15

SEQ ID NO:90:

Arg Glu Leu His Met Gly Pro Gly Arg Ala Arg Pro Gly Phe
1 5 10

SEQ ID NO:91:

Cys Arg Val Asp Phe Gly Pro Gly Arg Leu Gly Ser Arg Thr
1 5 10

SEQ ID NO:92:

Asn Val Val Ala Ile Gly Pro Gly Arg Ser Asn Val Val Thr
1 5 10

SEQ ID NO:93:

Lys Glu Val His Phe Gly Pro Gly Arg Gly Gly Gln Arg Ser
1 5 10

SEQ ID NO:94:

Xaa Xaa Tyr Leu Ile Gly Pro Gly Arg Gly Trp Glu Arg Glu
1 5 10

SEQ ID NO:95:

Ala Gly Cys Gln Val Gly Pro Gly Arg Pro Xaa Cys Gly Lys
1 5 10

SEQ ID NO:97:

Ile Gly Arg Asn Leu Gly Pro Gly Arg Val Val Ser Asn Val
1 5 10

SEQ ID NO:98:

Lys Asn Val His Val Gly Pro Gly Arg Gly Gln Arg Thr Val
1 5 10

SEQ ID NO:100:

Ser Lys Val Glu Ile Gly Pro Gly Arg Gly Pro Leu Met Arg
1 5 10

SEQ ID NO:102:

Gly Arg Ile Asn Tyr Gly Pro Gly Ala Pro Gly Leu Met
1 5 10

SEQ ID NO:103:

Glu Val His Tyr Tyr Gly Pro Gly Arg Arg Ala Pro Ala Ser
1 5 10

SEQ ID NO:104:

Val Glu Arg His Leu Gly Pro Gly Arg Gly Leu Gln Met Gly
1 5 10

SEQ ID NO:105:

Asn Ser Phe His Leu Gly Pro Gly Arg Ser Arg Thr Tyr Ser
1 5 10

SEQ ID NO:106:

Gly Val Val Lys Leu Gly Pro Gly Arg Thr Ala Gly Lys Leu
1 5 10

SEQ ID NO:107:

Leu Ile Gly Pro Gly Arg Ser Ser Val Ala Met Thr Ile Arg Glu
1 5 10 15

SEQ ID NO:108:

Leu Val Arg Met Leu Gly Pro Gly Arg Gly Asn Asp Arg Thr His
1 5 10 15

SEQ ID NO:109:

Gln Arg Gly Lys Thr Phe Tyr Gly Pro Gly Arg Gly Ser Gly Gln
1 5 10 15

SEQ ID NO:110:

Asp Arg Gly Lys Ile Val Tyr Gly Pro Gly Arg Thr Gln Ser
1 5 10

SEQ ID NO:112:

Gly Phe Ser Ser Ser Arg Val Leu Val Gly Pro Gly Arg Gly Val
1 5 10 15

SEQ ID NO:113:

Val Lys Arg Arg Asp Ala Val His Ala Gly Pro Gly
1 5 10

SEQ ID NO:114:

Asp Ser Glu Arg Val Gly Val Leu Leu Gly Pro Gly Arg Gly Val
1 5 10 15

SEQ ID NO:115:

Asp Leu Gly Arg Pro Ala Val Arg Phe Gly Pro Gly Arg Ile Ile
1 5 10 15

SEQ ID NO:116:

Leu Ser Arg Phe Arg Glu Trp His Val Gly Pro Gly Arg Val Pro
1 5 10 15

SEQ ID NO:118:

Ile Gly Val Thr Arg Ala Leu Phe Phe Gly Pro Gly Arg Gly Thr
1 5 10 15

SEQ ID NO:119:

Ser Leu Ser Arg Ala His Val His Arg Gly Pro Gly Arg Val Ser
1 5 10 15

SEQ ID NO:120:

Leu Val Tyr Arg Ala Ala His Tyr Gly Pro Gly Arg Gly Val
1 5 10

SEQ ID NO:121:

Arg Gly Trp Arg Pro Val Leu Ala Val Gly Pro Gly Arg Trp Glu
1 5 10 15

SEQ ID NO:134:

Cys Arg Ser Val His Leu Gly Pro Gly Arg Gly Asp Gly Leu Gly
1 5 10 15

Cys

SEQ ID NO:135:

Arg Ser Val His Leu Gly Pro Gly Arg Gly Asp Gly Leu Gly
1 5 10

SEQ ID NO:136:

Asp Gly Ser Arg Arg Ala Val His Leu Gly Pro Gly Arg Gly Val
1 5 10 15

SEQ ID NO:137:

Leu Leu Lys Glu Val His Phe Gly Pro Gly Arg Gly Arg Gly Gly
1 5 10 15

Arg Leu Leu

SEQ ID NO:138:

Cys Arg Gly Val His Leu Gly Pro Gly Arg Gly Ala Arg Met Ser
1 5 10 15

Cys

SEQ ID NO:139:

Cys Asp Arg Gly Ser Val Leu Ile Gly Pro Gly Arg Gly Ser Ser Xaa
1 5 10 15

Gly Cys

SEQ ID NO:140:

Asp Leu Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Ser Pro
1 5 10 15

Arg Ser

SEQ ID NO:141:

Cys Asp Leu Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Ser
1 5 10 15

Pro Arg Ser Cys
20

SEQ ID NO:142:

Asp Ser Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Glu Gly
1 5 10 15

Leu Ser

SEQ ID NO:143:

Cys Asp Ser Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Glu
1 5 10 15

Gly Leu Ser Cys
20

SEQ ID NO:144:

Trp Arg Ser Val His Leu Gly Pro Gly Arg Gly Ser Gly Ser
1 5 10

SEQ ID NO:145:

Cys Trp Arg Ser Val His Leu Gly Pro Gly Arg Gly Ser Gly Ser Cys
1 5 10 15

SEQ ID NO:1:

Pro Arg Leu Glu Thr His Phe Gly Pro Lys Arg Ser His Val Gly
1 5 10 15

SEQ ID NO:4:

Val Leu Val Trp Gln Arg Lys Val Phe Phe Gly Pro His Arg Ser
1 5 10 15

SEQ ID NO:5:

Arg Ser Ser Ser Trp Ala Trp Arg His Leu Tyr Gly Pro Ala Arg
1 5 10 15

SEQ ID NO:7:

Trp Asp Arg Gly Asn Ser Ser Gly Arg His Leu Gly Pro Ala Arg
1 5 10 15

SEQ ID NO:9:

Thr Trp His Leu Arg Val Arg Gly Ala His Phe Gly Pro Ala Arg
1 5 10 15

SEQ ID NO:10:

Trp Leu Arg Val Leu Leu Gly Pro Ala Arg Pro Ile Tyr Trp Arg
1 5 10 15

SEQ ID NO:11:

Leu Leu Leu Gly Pro Ala Arg Ala Pro Val Arg Val Asn Leu Ala
1 5 10 15

SEQ ID NO:12:

Cys Lys Pro Arg Ala Pro Met Leu Phe Gly Pro Ala Arg Gly Leu
1 5 10 15

SEQ ID NO:14:

Val Phe Lys Val Ile Asn Arg Ile Leu His Tyr Gly Pro Asn Arg
1 5 10 15

SEQ ID NO:16:

Asp Val Gly Trp Val Thr Gly Thr Gln His Tyr Gly Pro Arg Arg
1 5 10 15

SEQ ID NO:17:

Gly Leu Tyr Thr Cys Met Tyr Gly Pro Ser Arg His Ile Cys Val
1 5 10 15

SEQ ID NO:20:

Thr Glu Leu Gly Arg Gly Tyr Ile Ser His Gly Pro Ala Arg Gly
1 5 10 15

SEQ ID NO:22:

His Leu Gly Pro Ser Arg Gly Ala Asn Leu Gly Lys Ile Gly Ala
1 5 10 15

SEQ ID NO:24:

Leu His Val Gly Pro Asn Arg Gly Lys Ser Glu Asp Asn Tyr Arg
1 5 10 15

SEQ ID NO:27:

Phe Tyr Thr Ser Gly Lys Thr Ile Phe Tyr Tyr Gly Pro Arg Arg
1 5 10 15

SEQ ID NO:29:

Ala Cys Trp Ser Arg Glu Tyr Gly Pro Ala Arg Met Ser Cys Thr
1 5 10 15

SEQ ID NO:37:

Trp Ser Trp Val Arg Leu Lys Ala Val Leu Leu Gly Pro Ser Arg
1 5 10 15

SEQ ID NO:42:

Val Leu Arg Cys Phe Gly Pro Leu Arg Asp Ala Arg Cys Ser Val
1 5 10 15

SEQ ID NO:44:

Leu Met Val Val Gln Val Gly Pro Ala Arg Thr Phe Leu Gln Gly
1 5 10 15

SEQ ID NO:45:

Gly Pro Ser Leu Phe Asn Ser Gly Val Arg Tyr Gly Pro Lys Arg
1 5 10 15

SEQ ID NO:46:

Val His Phe Ile Gly Pro Gln Arg Gly Gly Asn Ser Ser His Leu
1 5 10 15

SEQ ID NO:53:

Met Glu Arg Asp Leu Val Arg Phe Gly Pro Asn Arg Asp Trp Arg
1 5 10 15

SEQ ID NO:54:

Asn Gly Leu Lys Leu Cys Arg Val Gly Pro Ser Arg Glu Gly Cys
1 5 10 15

SEQ ID NO:56:

Pro Val Lys Phe Gly Pro Gln Arg Ser Gly Gly Ala Thr Arg Pro
1 5 10 15

SEQ ID NO:57:

Ile Thr Pro Arg Leu Tyr Gly Pro Ser Arg Met Arg Tyr Asn Gln
1 5 10 15

SEQ ID NO:59:

Asn Lys Arg Glu Phe Gly Pro Ala Arg Ala Ala Arg Asn Arg
1 5 10

SEQ ID NO:60:

His Arg Arg Asp Ile Gly Pro Ala Arg Thr Arg Glu Ile Gly
1 5 10

SEQ ID NO:62:

Ser Ala Val His Leu Gly Pro Gln Arg Gln Arg Ala Thr Asp
1 5 10

SEQ ID NO:80:

Lys Gln Val Arg Leu Gly Pro Ala Arg Gly Asp Ile Ile Gly
1 5 10

SEQ ID NO:82:

Arg Ser Val Leu Met Gly Pro Ala Arg Ser Thr Arg Val Val
1 5 10

SEQ ID NO:87:

Gln His Arg Ala Ala Ser Val His Leu Gly Pro Ser Arg Ala Gly
1 5 10 15

SEQ ID NO:88:

Leu Met Phe Val Arg Val Val Lys Leu Gly Pro Ala Arg Val Pro
1 5 10 15

SEQ ID NO:89:

Tyr Gly Leu Val Ile Arg Cys Glu Val Gly Pro Ser Arg Ser Cys
1 5 10 15

SEQ ID NO:96:

Arg Glu Val His Phe Gly Pro Arg Arg Asp Glu Pro Gly Arg
1 5 10

SEQ ID NO:99:

Arg Leu His Leu Val Gly Pro Ala Arg Val Ser Pro Leu Ser
1 5 10

SEQ ID NO:101:

Ala Val Ile His Val Gly Pro Ser Arg Leu Lys Ser Gln Tyr
1 5 10

SEQ ID NO:111:

Asp Trp Arg Ser Val His Ile Gly Pro Ala Arg Arg Glu Val Leu
1 5 10 15

SEQ ID NO:117:

Ala Ala Leu Arg Lys Val Arg Xaa Tyr Gly Pro Ala Arg Gln Ser
1 5 10 15

The new SPNE amino acid sequences of this invention include any fragment thereof in the sequence listing, provided said fragment is at least five amino acids in length, and includes the GPXR (SEQ. ID NO:123) loop region or homolog.

Each SPNE amino acid sequence can be determined by DNA sequencing of phage clones amplified by the polymerase chain reaction.

The present invention also provides an effective immunogen against AIDS or ARC, and comprises an antigenic conjugate of the formula

$$(SPNE)_n\text{-}(OMPC) \qquad I,$$

wherein:

SPNE is the selected principal neutralization epitope of HIV, which is a polypeptide of one or more amino acid sequences, each sequence having any of sequences of Table A, or fragments thereof, said fragment having at least 5 amino acids in length and including the GPXR loop region or homolog thereof;

n = 1-50, wherein n is the number of polypeptides of SPNE covalently linked to OMPC;

~ indicates covalent linkage;

OMPC is outer membrane proteosome of the micro-organism Neisseria,

said conjugate optionally substituted with an anion or polyanion to render it soluble such as polyproprionic acid, or substituted with a- which is an anion or polyanion at physiological pH, said a- consisting of one to five residues of

anions selected from the group consisting of carboxylic, sulfonic, proprionic or phosphonic acid, or pharmaceutically acceptable salts.

Each conjugate molecule of formula I may have different peptides conjugated thereto, or, alternatively, multiples of a single peptide species conjugated thereto, or a combination.

The antigenic conjugates of this invention are prepared by isolating, synthesizing and purifying their component parts SPNE and OMPC, then conjugating SPNE and OMPC together. Subsequent purification of conjugate mixtures may be performed as desired.

Applicants also have developed a method for identifying new SPNE by the screening of phage libraries bearing randomly or semi randomly generated oligopeptide epitopes. The library is screened with any antibody, and is specifically illustrated by screening with a broadly neutralizing monoclonal antibody.

Polymerase Chain Reaction Amplification

Large amounts of DNA coding for SPNE protein may be obtained using polymerase chain reaction (PCR) amplification techniques as described in Mullins et al., U.S. Patent No. 4,800,159 and other published sources. See also, for example, Innis, M.A. et al. PCR Protocols Academic Press 1990. The extension product of one primer, when hybridized to another primer, becomes a template for the synthesis of another nucleic acid molecule.

The primer template complexes act as substrate for DNA polymerase which, in performing its replication function, extends the primers. The region in common with both primer extensions, upon denaturation, serves as template for a repeated primer extension.

Taq DNA Polymerase catalyzes primer extension in the amplification process. The enzyme is a thermostable DNA polymerase isolated from Thermus aquaticus. Because it stays active through repeated elevations to high denaturation temperatures, it needs to be added only once. Deoxynucleotide triphosphates provide the building blocks for primer extension.

The nucleic acid sequence strands are heated until they separate, in the presence of oligonucleotide primers that bind to their complementary strand at a particular site on the template. This process is continued with a series of heating and cooling cycles, heating to separate strands, and cooling to reanneal and extend the sequences. More and more copies of the strands are generated as the cycle is repeated. Through amplification, the coding domain and any additional primer-encoded information such as restriction sites or translation signals (signal sequences, start codons and/or stop codons) is obtained. PCR protocols are often performed at the 100 µL scale in 0.5 ml microcentrifuge tubes. The PCR sample may be single- or double-stranded DNA or RNA. If the starting material is RNA, reverse transcriptase is used to prepare first strand cDNA prior

to PCR. Typically, nanogram amounts of cloned template, up to microgram amounts of genomic DNA, or 20,000 target copies are chosen to start optimization trials.

PCR primers are oligonucleotides, typically 15 to 50 bases long, and are complementary to sequences defining the 5' ends of the complementary template strands. Non-template complementary 5' extensions may be added to primers to allow a variety of useful post amplification operations on the PCR product without significant perturbation of the amplification itself. It is important that the two PCR primers not contain more than two bases complementary with each other, especially at their 3' ends. Internal secondary structure should be avoided in primers.

Because Taq DNA Polymerase has activity in the 37-55°C range, primer extension will occur during the annealing step and the hybrid will be stabilized. The concentrations of the primers are preferably equal in conventional PCR and, typically, are in vast excess of the template to be reproduced.

In one typical PCR protocol, each deoxy-nucleotide triphosphate concentration is preferably about 200 μM. The four dNTP concentrations are preferably above the estimated Km of each dNTP (10-15 μM).

Preferably PCR buffer is composed of about 50 mM potassium chloride, 10.0 mM Tris-HCl (pH 8.3 at room temperature), 1.5 mM magnesium chloride, and 0.001% w/v gelatin. In the presence of 0.8 mM total dNTP concentration, a titration series in small

increments over the 1.5-to 4-mM range will locate the magnesium concentration producing the highest yield of a specific product. Too little free magnesium will result in no PCR product and too much free magnesium may produce a variety of unwanted products.

Preferably, in a 100-µL reaction volume, 2.0 to 2.5 units of Taq DNA Polymerase are recommended. The enzyme can be added conveniently to a fresh master mix prepared for a number of reactions, thereby avoiding accuracy problems associated with adding individual 0.5-µL enzyme aliquots to each tube. A typical PCR protocol for amplification of the DNA template includes an initial 8 minute 94°C denaturation step, followed by 30 cycles of 30 seconds at 94°C (denaturation), 1 minute at 55°C (primer annealing), and 2 minutes at 72°C (polymerization). At the end of the last cycle, all strands are completed by a 5 minute incubation at 72°C.

During DNA denaturation, sufficient time must be allowed for thermal equilibration of the sample. The practical range of effective denaturation temperatures for most samples is 92-95°C, with 94°C being the standard choice.

Primer annealing is usually performed first at 55°C, and the specificity of the product is evaluated. If unwanted bands are observed, the annealing temperature should be raised in subsequent optimization runs. While the primer annealing temperature range is often 37-55°C, it may be raised as high as the extension temperature in some cases. Merging of the primer annealing and primer extension steps results in a two-step PCR process.

Primer extension, in most applications, occurs effectively at a temperature of 72°C and seldom needs optimization. In the two-temperature PCR process the temperature range may be 65-70°C. In situations where enzyme concentration limits amplification in late cycles, the extension is preferably increased linearly with cyclic number. Usually, 25 to 45 cycles are required for extensive amplification (i.e., 1,000,000 fold) of a specific target.

Once the DNA sequence is determined, through conventional and well-known techniques, its amino acid sequence can be deduced by "translating" the DNA sequence. The resulting amino acid sequence having the selected principal neutralizing epitope of the envelope gene is then employed to synthesize large quantities of SPNE protein or fragment thereof. Synthesis is performed by organic synthesis or by recombinant expression systems, or both.

Preparation of Selected Principal Neutralization Epitope

A. Organic Synthesis of SPNE:

Standard and conventional methods exist for rapid and accurate synthesis of long peptides on solid-phase supports. Solution-phase synthesis is usually feasible only for selected smaller peptides.

Synthesis on solid-phase supports, or solid-phase synthesis, is most conveniently performed on an automated peptide synthesizer according to

e.g., Kent, S. et al., "Modern Methods for the Chemical Synthesis of Biologically Active Peptides," in Alitalo, K. et al., (eds.). Synthetic Peptides in Biology and Medicine, Elsevier 1985, pp. 29-57. Manual solid-phase synthesis may be employed instead, by following the classical Merrifield techniques, as described, for example, in Merrifield, R.B. J. Am. Chem. Soc. 85, 2149 (1963), or known improvements thereof. Solid-phase peptide synthesis may also be performed by the Fmoc method, which employs very dilute base to remove the Fmoc protecting group. Segment synthesis-condensation is a further variant of organic synthesis of peptides as within the scope of the techniques of the present invention.

In organic synthesis of peptides, protected amino acids are condensed to form amide or peptide bonds with the N-terminus of a growing peptide. Condensation is usually performed with the carbodiimide method by reagents such as dicyclohexylcarbodiimide, or N-ethyl, N_1-(γ-dimethylaminopropyl) carbodiimide. Other methods of forming the amide or peptide bond include, but are not limited to, synthetic routes via an acid chloride, azide, mixed anhydride or activated ester. Common solid-phase supports include polystyrene or polyamide resins.

The selection of protecting groups of amino acid side chains is, in part, dictated by particular coupling conditions, in part by the amino acid and peptide components involved in the reaction. Such amino-protecting groups ordinarily employed include those which are well known in the art, for example,

urethane protecting substituents such as benzyloxy-carbonyl (carbobenzoxy), p-methoxycarbobenzoxy, p-nitrocarbobenzoxy, t-butyloxycarbonyl, and the like. It is preferred to utilize t-butoxycarbonyl (BOC) for protecting the ε-amino group, in part because the BOC protecting group is readily removed by relatively mild acids such as trifluoroacetic acid (TFA), or hydrogen chloride in ethyl acetate.

The OH group of Thr and Ser may be protected by the Bzl (benzyl) group and the ε-amino group of Lys may be protected by the isopropoxycarbonyl (IPOC) group or the 2-chlorobenzyloxycarbonyl (2-Cl-CBZ) group. Treatment with hydrogen fluoride or catalytic hydrogenation are typically employed for removal of IPOC or 2-Cl-CBZ.

For preparing cocktails of closely related peptides, see, e.g., Houghton, R.A., Proc. Natl. Acad. Sci. USA 82, 5131 (1985).

B. Expression of SPNE in a Recombinant Expression System

It is now a relatively straightforward technology to prepare cells expressing a foreign gene. Such cells act as hosts and include E. coli, B. subtilis, yeasts, fungi, plant cells or animal cells. Expression vectors for many of these host cells have been isolated and characterized, and are used as starting materials in the construction, through conventional recombinant DNA techniques, of vectors having a foreign DNA insert of interest. Any DNA is foreign if it does not naturally derive from the host cells used to express the DNA insert. The

foreign DNA insert may be expressed on extra-chromosomal plasmids or after integration in whole or in part in the host cell chromosome(s), or may actually exist in the host cell as a combination of more than one molecular form. The choice of host cell and expression vector for the expression of a desired foreign DNA largely depends on availability of the host cell and how fastidious it is, whether the host cell will support the replication of the expression vector, and other factors readily appreciated by those of ordinary skill in the art.

The technology for recombinant procaryotic expression systems is now old and conventional. The typical host cell is E. coli. The technology is illustrated by treatises such as Wu, R (ed) Meth. Enzymol. 68 (1979) and Maniatis, T. et. al., Molecular Cloning: A Laboratory Manual Cold Spring Harbor 1982.

The foreign DNA insert of interest comprises any DNA sequence coding for a SPNE (or fragment thereof of at least 5 amino acids in length) of the present invention, including any synthetic sequence with this coding capacity or any such cloned sequence or combination thereof. For example, SPNE peptides coded and expressed by an entirely recombinant DNA sequence is encompassed by this invention.

Vectors useful for constructing eukaryotic expression systems for the production of recombinant SPNE comprise the DNA sequence for SPNE, fragment or variant thereof, operatively linked thereto with appropriate transcriptional activation DNA sequences, such as a promoter and/or operator. Other typical

features may include appropriate ribosome binding sites, termination codons, enhancers, terminators, or replicon elements. These additional features can be inserted into the vector at the appropriate site or sites by conventional splicing techniques such as restriction endonuclease digestion and ligation.

Yeast expression systems, which are one variety of recombinant eukaryotic expression systems, generally employ Saccharomyces cerevisiae as the species of choice for expressing recombinant proteins. S. cerevisiae and similar yeasts possess well known promoters useful in the construction of yeast expression systems, including but not limited to GAP491, GAL10, ADH2, and alpha mating factor.

Yeast vectors useful for constructing recombinant yeast expression systems for expressing SPNE include, but are not limited to, shuttle vectors, cosmids, chimeric plasmids, and those having sequences derived from 2-micron circle plasmids.

Insertion of the appropriate DNA sequence coding for SPNE, fragment or variant thereof, into these vectors will, in principle, result in a useful recombinant yeast expression system for SPNE where the modified vector is inserted into the appropriate host cell, by transformation or other means.

Recombinant mammalian expression systems are another means of producing the recombinant SPNE for the conjugates of this invention. In general, a host mammalian cell can be any cell that has been efficiently cloned in cell culture. Host mammalian cells useful for the purposes of constructing a recombinant mammalian expression system include, but

are not limited to, Vero cells, NIH3T3, GH3, COS, murine C127 or mouse L cells. Mammalian expression vectors can be based on virus vectors, plasmid vectors which may have SV40, BPV or other viral replicons, or vectors without a replicon for animal cells. Detailed discussions on mammalian expression vectors can be found in the treatises of Glover, D.M. (ed.) "DNA Cloning: A Practical Approach," IRL 1985, Vols. I and II.

Recombinant SPNE may possess additional and desirable structural modifications not shared with the same organically synthesized peptide, such as adenylation, carboxylation, glycosylation, hydroxylation, methylation, phosphorylation or myristoylation. These added features may be chosen or preferred as the case may be, by the appropriate choice of recombinant expression system. On the other hand, recombinant SPNE may have its sequence extended by the principles and practice of organic synthesis of section A above.

Conjugation of SPNE and OMPC to Form a Covalent Linkage(s) Yielding Conjugate or Coconjugate

Antigenic conjugates of SPNE and OMPC are useful for vaccination against AIDS or ARC. Such conjugates have at least one covalent linkage between the antigen SPNE and OMPC, and typically have more than one SPNE molecule covalently bound to each OMPC molecule.

SPNE and OMPC are prepared separately, then linked by non-specific cross-linking agents,

monogeneric spacers or bigeneric spacers. Methods for non-specific cross-linking include, but are not limited to, reaction with glutaraldehyde; reaction with N-ethyl-N'-(3-dimethylaminopropyl) carbodiimide, with or without admixture of a succinylated carrier; periodate oxidation of glycosylated substituents followed by coupling to free amino groups of a protein carrier in the presence of sodium borohydride or sodium cyanoborohydride; diazotization of aromatic amino groups followed by coupling on tyrosine side chain residues of the protein; reaction with isocyanates; or reaction of mixed anhydrides. See, generally, Briand, J.P. et al. J. Imm. Meth. 78, 59 (1985). These methods of non-specifically cross-linking are conventional and well-known in the typical practice of preparing conjugates for immunological purposes.

In another embodiment of the invention, conjugates formed with a monogeneric spacer are prepared. These spacers are bifunctional and require functionalization of only one of the partners of the reaction pair to be conjugated before conjugation takes place.

By way of illustration rather than limitation, an example of a monogeneric spacer involves coupling the polypeptide SPNE to one end of the bifunctional molecule adipic acid dihydrazide in the presence of carbodiimide. A diacylated hydrazine presumably forms with pendant glutamic or aspartic carboxyl groups of SPNE. Conjugation then is performed by a second coupling reaction with carrier protein in the presence of carbodiimide. For similar

procedures, see for example, Schneerson, R. et al., J. Exp. Med. 152, 361 (1980). Another example of a monogeneric spacer is described in Fujii, N. et al. Int. J. Peptide Protein Res. 26, 121 (1985).

In another embodiment of the invention, conjugates of SPNE and OMPC are formed with a bigeneric spacer. These spacers are formed after each partner of the reaction pair to be conjugated, e.g., SPNE and OMPC, is functionalized with a bifunctional spacer. Conjugation occurs when each functionalized partner is reacted with its opposite partner to form a stable covalent bond or bonds. See, for example, Marburg, S. et al., J. Am. Chem. Soc. 108, 5282-5287 (1986) and Marburg, S. et al., U.S. Patent 4,695,624, issued 22 September 1987. Bigeneric spacers are preferred for preparing conjugates in human vaccines since the conjugation reaction is well characterized and easily controlled.

In another embodiment of this invention, coconjugates are formed of SPNE and OMPC, comprising conjugates of SPNE and OMPC wherein OMPC is also covalently modified with a low molecular weight moiety (hereinafter a-) having an anionic or polyanionic character at physiological pH. The term a- is typically one to five residues of an anionic form of carboxylic, sulfonic, proprionic or phosphonic acid. Such coconjugates are suitable for raising an anti-SPNE response, since the anions enhance solubility of conjugates in aqueous solutions. Their synthesis, detailed description and other advantages are described in EP0467700 of Leanza, W.J. et al.

Typical and conventional immunological practice provides for the ready and easy synthesis of antigenic conjugates within the scope of the present invention, including the conjugation of OMPC with virtually any desired degree of substitution of virtually any peptide of the Sequence Listing. Heterogeneous products of the conjugation reaction are easily separable if needed by a variety of suitable column chromatography techniques.

Recombinant Fusion Polypeptides (RFPs)

For ease in evaluating SPNE as immunogens, applicants have contructed recombinent shuttle vectors coding for RFPs of novel SPNE and selected peptides or fragments thereof, such as pIII (with or without a polyhistidine tail), Hep B core, Hep B surface antigen or protein A. The methods for contruction of fusion peptides are well known in the art. Coding sequences are prepared by ligation of other sequences, cloning, PCR, mutagenesis, organic synthesis, or combination thereof, in accordance with the principles and practice of constructing DNA sequences.

For the particular RFPs of this invention, DNA sequences coding for a selected SPNE are ligated in frame to DNA sequences coding for pIII, Hep B core or protein A. The resulting DNA fragment is expressed in any one of a wide variety of readily available recombinant expression systems, e.g. *E. coli* BL21 (DE3), as also discussed in the Examples and in the section on expression of SPNE in a recombinant expression system, above.

In the alternative, the fusion peptides can be made by synthetic organic means, although this method is limited by feasibility and by practicality to smaller fusion peptides. See also the section on organic synthesis of SPNE, above.

Vaccine Formulation

The form of the immunogen within the vaccine takes various molecular configurations. A single molecular species of the antigenic conjugate $(SPNE)_n$-OMPC will often suffice as a useful and suitable antigen for the prevention or treatment of AIDS or ARC. Other antigens in the form of cocktails are also advantageous, and consist of a mixture of conjugates that differ by, for example, the degree of substitution (n) or the amino acid sequence of SPNE or both.

An immunological vector or adjuvant may be added as an immunological vehicle according to conventional immunological testing or practice.

The conjugates of this invention when used as a vaccine, are to be administered in immunologically effective amounts. Dosages of between 1 µg and 500 µg of conjugate, and preferably between 50 µg and 300 µg of conjugate are to be administered to a mammal to induce anti-peptide, anti-HIV, or HIV-neutralizing immune responses. About two weeks after the initial administration, a booster dose may be administered, and then again whenever serum antibody titers diminish. The conjugate should be given intramuscularly at a concentration of between 10 µg/ml and 1 mg/ml, and

preferably between 50 and 500 μg/ml, in a volume sufficient to make up the total required for immunological efficacy.

Adjuvants may or may not be added during the preparation of the vaccines of this invention. Alum is the typical and preferred adjuvant in human vaccines, especially in the form of a thixotropic, viscous, and homogeneous aluminum hydroxide gel. For example, one embodiment of the present invention is the prophylactic vaccination of patients with a suspension of alum adjuvant as vehicle and a cocktail of $(SPNE)_n$-OMPC as the selected set of immunogens or antigens.

Other Utilitites

The SPNEs and their immunological conjugates in this invention are also useful in screening blood products for the presence of HIV antigen or HIV-specific antibody. Thus, $(SPNE)_n$-OMPC or SPNE can be readily employed in a variety of immunological assays of the type well known to the skilled artisan, e.g., radioimmunoassay, competitive radioimmunoassay, enzyme-linked immunoassay, and the like. For an extensive discussion of these types of utilities, see, e.g. U.S. 5,075,211.

Method for Screening Phage Epitope Libraries

Phage epitope libraries are unusually versatile vehicles for identifying new antigens or ligands. Typically, the phage has inserted into its genome a small, randomly generated DNA sequence, e.g. 45 base pairs, which will generate exposed oligo-peptide surfaces in the mature phage. Mixing a

library of such mature phage with a screening antibody of desired specificity, followed by separation of bound from unbound phage, allows the opportunity to clone and sequence the bound phage. A conventional example of a phage epitope library is the filamentous phage fd and its gene III coding for minor coat protein pIII. See, e.g., Parmley, S. F. et al. Gene 73, 305 (1988) and Scott, J. K. et al. Science 249, 386 (1990), which set forth extensive discussion and detail on construction of these libraries.

Applicants have developed a new method for screening phage epitope libraries. The screening method involves selection of epitopes by binding to a solid-phase supported antibody, optionally followed by identification of desired clones with antibody lifts. The screening method is useful for virtually any antibody, i.e. polyclonal or monoclonal or collection of monoclonals thereto. Any antigen can be screened. The screening method is illustrated by HIV antigens screened with an HIV-specific broadly neutralizing antibody (hereinafter 447 antibody).

The present screening method avoids the typical prior art problem of biotin-avidin complexes. Although, biotin-avidin complex formation has an unusually high binding constant, it produces false positives, is time-consuming, and requires tampering with the antibody by covalent conjugation. Applicants avoid all of these problems by adsorbing the antibody onto a solid-phase support. With a particular series of mixing and washing steps, applicants demonstrate a practical method of screening phage libraries.

Screening in the present invention is broken down into two separate methods. The first method involves selection of desired phage epitopes with a solid-phase supported antibody of any desired specificity. The second method, which is optional, relates to identification of desired phage epitopes by antibody lifts.

A. Selection

Selection of desired phage epitopes in a phage epitope library is performed as follows. An essentially pure preparation of monospecific antibody is adsorbed or otherwise attached to a solid-phase support, hereinafter also referred to as solid-phase supported Ab. The most preferred embodiment is monoclonal antibody adsorbed to polystyrene beads large enough to be picked up with tweezers, e.g., with a diameter of 0.25 inch. Such large beads contribute to the ease of subsequent washing steps. Other embodiments include any solid-phase adsorbent for antibody, or any plastic, or glass bead or polysaccharide gel, e.g. Sepharose. Polysaccharide gels are typically covalently conjugated to the purified antibody by, e.g., cyanogen bromide activation.

Incubation of the solid-phase supported Ab with BSA, milk solids or other reagent for blocking non-specific interactions is preferable before selection. The presence of low levels of a mild or nonionic detergent is desirable, e.g., 0.5%(v/v) of

one or more in the polyoxyethylene (20) sorbitan monoleate series (TWEEN), or octylglucopyranoside or Nonidet NP-40. It is apparent to the skilled how to adjust the conditions for coating with such blocking agents.

An appropriate density of antibody should be determined by titration. Applicants have successfully performed selection with a density of about 0.1 μg447/cm^2 on polystyrene beads (d = 0.25 inch). This falls within a preferred density range of between about 1μg Ab/cm^2 and about 1ng Ab/cm^2. Densities in the lower range select high affinity epitopes because of the reduced incidence of multivalent binding by the antibody to the multiple copies of the epitope on the phage tip. It is apparent to the skilled artisan how to determine the most suitable density for an antibody preparation, by monitoring the bound phage population. As a general rule, a manageable complexity of bound and eluted phage ranges from about $5x10^3$ to about 10^5 phage.

Throughout the selection method described below, a wide variation in incubation times, washing times, temperature and pH is covered. It is apparent to the skilled artisan that, given a particular incubation or washing step, a suitable set of variant reaction conditions can be readily ascertained. Applicants have discovered that temperature and pH are critical in the stringent selection of high affinity epitopes, e.g., temperatures exceeding about 70°C at neutral pH, or exceeding about 38°C at pH

4.0, are lethal to the phage. Aside from the critical parameters of temperature and pH, the typical buffer is isotonic to saline, and may contain a non-specific blocking agent such as bovine serum albumin (BSA) or milk solids, as well as low levels of a nonionic detergent. For example, TTBS (50mM Tris pH 7.5, 150 mM NaCl, 0.5% (v/v) TWEEN-20) in 1mg/ml BSA is typical.

Solid-phase supported antibody is first incubated with the epitope phage library to effect binding of the phage epitopes to the antibody. It is preferred to use enough phage to vastly exceed the library complexity, e.g., 10^{11} phage which is 1000 fold more than its complexity of 10^{8}. Incubation between about 4°C and about 65°C, for at least 10 minutes is performed. Applicants typically incubate overnight at 4°C. Alternatively, a one hour incubation at 37°C will select epitopes binding at a fast "on" or forward rate. Incubation conditions are subject to a wide range of variations, as also discussed above, but a neutral buffer containing a non-specific blocking agent is preferred, e.g., TTBS, 1 mg/ml BSA.

Washing of the mixture of phage epitope library and solid-phase supported antibody to remove unbound phage is carried out in a variety of conditions, depending on the desired stringency. The higher the desired stringency, the higher the temperature conditions of washing, up to 70°C in some conditions.

For high stringency selection, washing of the mixture is carried out by washing 3 to 20 times in buffer at neutral pH at 65°C without blocking agent (hereinafter the 65°C wash). Low-affinity phage epitopes are then eluted by washing one or more times by brief (2-5 minutes) immersion in a mildly acidic buffer without blocking agent (about pH 4.0, between 5.0 and 3.0) at ambient temperature or between about 4°C and 37°C (the pH 4.0 wash). The pH 4.0 wash is optional in high stringency selection, but it cannot be completely combined with the 65°C wash. For example, the phage die in pH 4.0 buffer at 65°C.

High stringency selection may be enhanced by lowering the antibody density on the bead or other solid-phase support. In this case, lowering the probability that a given phage will bind more than one antibody molecule selects for higher affinity epitopes. It will be apparent to those skilled in the art how to test density variations within the aforementioned ranges.

Lower stringency selection is performed instead by washing 3 to 20 times at neutral pH at about room temperature. A pH 4.0 wash may optionally follow.

Elution of high affinity epitopes is the next required step (hereinafter the pH 2.0 elution) for both high and low stringency selection. Phage bound to solid-phase supported antibody are incubated briefly (1-15 minutes) in a low pH buffer in about 0.1-10 mg/ml BSA or other non-specific binder. The buffer pH can vary from about 2.3 to about 1.0, but 2.2 is preferred. Temperature conditions range from

about 37°C to 4°C, room temperature being desirable. Preferred buffered conditions are 0.1N glycine•HCl pH 2.2, 1 mg/ml BSA at room temperature.

After the pH 2.0 elution, the eluted solution containing phage is neutralized by standard and well-known techniques. The eluted phage are grown in infectable E. coli, e.g. tet^+ phage are grown in tet^- E.coli on media containing tetracycline.

Thus concludes one cycle of selection, either at high stringency or low stringency. Repetition of the cycle is often found advantageous, as it lowers the complexity of eluted phage to manageable quantities (less than about 10^5). Repeating the cycle 2-10 times, preferably 3-5 times, is found most practical. It will be apparent to those skilled in the art that indicated variations are readily performed and evaluated, such as switching from high stringency to low stringency on the second cycle of selection, or changing the buffer or its pH.

B. Identification With Antibody Lifts

After selection of epitopes bound to phage, it is advantageous to identify with antibody lifts those clones with desired epitopes. The principle is to overlay culture plates of cells infected with selected phage epitopes, remove the overlay, block the overlay, incubate the blocked overlay with desired antibody, label the bound antibody, and locate on the original culture plate those colonies that bind the antibody. Versions of this overlay technique that differ from the present method exist

in the literature. Methods known in the art are typically adopted for use with plaque formers, unlike the present invention. See, e.g., Young, R.A. et al., Proc Natl. Acad Sci 80, 1194 (1983); Ausubel, F.M. et al. (eds.), "Screening Recombinant DNA Libraries," in Current Protocols in Molecular Biology, Chapter 6, Greene 1989; and Davis, L.G. et al., Basic Methods in Molecular Biology, pp. 214-215, Elsevier 1986.

Plates having epitope phage-infected colonies are grown to the extent that the colonies are sufficiently large, i.e., between about 1mm and about 4mm in diameter, yielding mature plates.

Mature plates are overlaid with a disk that binds proteins. The disc is typically nitrocellulose, but it may also be IMMOBILON P, cellulose acetate and the like. The disk is immediately removed and subjected to further treatment.

Blocking the overlay or disk is first performed to eliminate or substantially reduce the background of non-specific interactions. Useful blocking agents include BSA, milk solids and similar proteinaceous preparations. The disks are soaked for at least 2 hours in buffer, containing between about 0.1% (v/v) and about 1.0% (v/v) neutral detergent and at least 1% blocking agent. One preferred embodiment for this blocking step is soaking for 4 hours each disk in TTBS, 10% evaporated milk, at room temperature. A preferred range is incubation for at least 2 hours, in a buffer near neutrality (5.0-8.0) containing 0.1% (v/v) - 1.0% (v/v) neutral detergent,

in about 1% to about 20% blocking agent, within a temperature range of about 4°C to about 80°C.

Washing the blocked disks to remove excess blocking agent follows, and is carried out in a buffer lacking the blocking agent. One preferred embodiment for this washing step is soaking each disk two or three times in TTBS, pH 7.3-7.5, at room temperature. A preferred range of conditions is soaking for at least 10 minutes, in a buffer with a pH that does not destroy antibody (5.0-8.0), containing 0.1% (v/v) to 1.0% (v/v) neutral detergent, within a temperature range of about 4°C to about 80°C.

Contacting the disk with screening antibody follows. One preferred embodiment is incubating the washed disks overnight at 4°C with gentle rocking, in TTBS, 1% evaporated milk, 0.5 to 1.0 µg/ml antibody. A preferred range of conditions is incubating the disks for at least 4 hours, within a temperature range of between about 4°C and about 65°C, in buffer near neutrality containing about 0.1% (v/v) to about 1.0% (v/v) neutral detergent, in 0.1% to 5% blocking agent, and 0.1 to 5 µg/ul antibody.

A second series of washes are performed, here to remove excess or unbound antibody. One preferred embodiment is soaking each disk four times in TTBS for 20 minutes at room temperature. Preferred ranges of conditions are at least 2 soaks in buffer without blocking agents at a pH near neutrality (6.0-8.0), for 5 minutes to 1 hour, between about 10°C and 45°C.

The resulting washed disks having bound antibody are treated with a labeled second-stage reagent to determine the location of the bound antibody and the corresponding epitope clone. Any labeled or tagged second-stage reagent useful for binding the bound antibody can in principle be incorporated into the procedure for the purposes of identifying the clones having epitopes bound by antibody. One preferred embodiment is soaking the washed disks having bound antibody in TTBS, 1% milk, ^{125}I-protein A (0.5 to 1μ curie/ml) for 1.5 to 3 hours. Preferred ranges of conditions are incubating the disks for at least 1 hour, within a temperature range of between about 4°C to about 65°C, in buffer near neutrality containing about 0.1% (v/v) to about 1.0% (v/v) neutral detergent, in about 0.1% to about 5% blocking agent and detectable quantities of labeled protein A. Another preferred second-stage reagent is labeled protein G, e.g., ^{125}I-protein G. Other appropriate second-stage reagents include, but are not limited to, double antibody, such as ^{125}I-labeled mouse anti-human IgG, or mouse anti-human IgG tagged with beta-galactosidase or peroxidase. Substantial purity of labeled second-stage reagent is desirable.

The disks having bound labeled antibody are now soaked or washed to remove unbound label. One preferred embodiment is soaking 20 minutes four times in TTBS. The location of the labeled, bound antibody on the disks is determined by conventional procedures appropriate for the labeled second-stage reagent.

X-ray film is used for ^{125}I. Chromogenic substrates are useful in a variety of enzyme-antibody detection kits.

Once the location of the bound antibody is determined, e.g., a pattern of dark spots on developed X-ray film, one identifies the appropriate colonies on the original mature plate, since regrown as needed. Subsequent replating, growth, and sequencing gives a particular selected principal neutralizing epitope (SPNE).

COMBINATION THERAPY

The vaccines of this invention may be effectively administered, whether at periods of pre-exposure and/or post-exposure, in combination with effective amounts of the AIDS antivirals, immunomodulators, anti-infectives, or vaccines of the following Table.

TABLE I

ANTI-VIRALS

Drug Name	Manufacturer	Indication
AL-721	Ethigen (Los Angeles, CA)	ARC, PGL HIV positive, AIDS
Recombinant Human Interferon Beta	Triton Biosciences (Almeda, CA)	AIDS, Kaposi's sarcoma, ARC
Acemannan	Carrington Labs (Irving, TX)	ARC (See also immuno-modulators)
Cytovene Ganciclovir	Syntex (Palo Alto, CA)	sight threateining CMV peripheral CMV retinitis
d4T Didehydrodeoxy-thymidine	Bristol-Myers (New York, NY)	AIDS, ARC
ddI Dideoxyinosine	Bristol-Myers (New York, NY)	AIDS, ARC
EL10	Elan Corp, PLC (Gainesville, GA)	HIV infection (See also immuno-modulators)
Foscarnet Trisodium Phosphonoformate	Astra Pharm. Products, Inc. (Westborough, MA)	CMV retinitis, HIV infection, other CMV infections

Drug Name	Manufacturer	Indication
L-697,661	Merck (Rahway, NJ)	AIDS, ARC, HIV positive asymptomatic, or in combination with AZT, ddC or ddI. Inhibitor of HIV RT
L-696,229	Merck (Rahway, NJ)	AIDS, ARC, HIV positive asymptomatic, or in combination with AZT, ddC or ddI. Inhibitor of HIV RT
L-735,524	Merck (Rahway, NJ)	AIDS, ARC, HIV positive asymptomatic, or in combination with AZT, ddC or ddI. Inhibitor of HIV Protease, not HIV RT
Dideoxycytidine; ddC	Hoffman-La Roche (Nutley, NJ)	AIDS, ARC
Novapren	Novaferon Labs, Inc. (Akron, OH) Diapren, Inc. (Roseville, MN, marketer)	HIV inhibitor

Drug Name	Manufacturer	Indication
Peptide T Octapeptide Sequence	Peninsula Labs (Belmont, CA)	AIDS
Retrovir Zidovudine; AZT	Burroughs Wellcome (Rsch. Triangle Park, NC)	AIDS, adv, ARC pediatric AIDS, Kaposi's sarcoma, asymptomatic HIV infection, less severe HIV disease, neurological involvement, in combination w/ other therapies, post-exposure prophylaxis in health care workers
Rifabutin Ansamycin LM 427	Adria Laboratories (Dublin, OH) Erbamont (Stamford, CT)	ARC
Dextran Sulfate	Ueno Fine Chem. Ind. Ltd. (Osaka, Japan)	AIDS, ARC, HIV positive asymptomatic
Virazole Ribavirin	Viratek/ICN (Costa Mesa, CA)	asymptomatic HIV positive, LAS, ARC
Alpha Interferon	Burroughs Wellcome (Rsch. Triangle Park, NC)	Kaposi's sarcoma, HIV in combination w/Retrovir

Immuno-modulators

Drug Name	Manufacturer	Indication
Antibody which neutralizes pH labile alpha aberrant Interferon in an immunoadsorption column	Advanced Biotherapy Concepts (Rockville, MD)	AIDS, ARC
AS-101	Wyeth-Ayerst Labs. (Philadelphia, PA)	AIDS
Bropirimine	Upjohn (Kalamazoo, MI)	advanced AIDS
Acemannan	Carrington Labs, Inc. (Irving, TX)	AIDS, ARC (See also antivirals)
CL246,738	American Cyanamid (Pearl River, NY) Lederle Labs (Wayne, NJ)	AIDS, Kaposi's sarcoma
EL10	Elan Corp, PLC (Gainesville, GA)	HIV infection (See also antivirals)
Gamma Interferon	Genentech (S. San Francisco, CA)	ARC, in combination w/TNF (tumor necrosis factor)

Drug Name	Manufacturer	Indication
Granulocyte Macrophage Colony Stimulating Factor	Genetics Institute (Cambridge, MA) Sandoz (East Hanover, NJ)	AIDS
Granulocyte Macrophage Colony Stimulating Factor	Hoeschst-Roussel (Somerville, NJ) Immunex (Seattle, WA)	AIDS
Granulocyte Macrophage Colony Stimulating Factor	Schering-Plough (Madison, NJ)	AIDS AIDS, in combination w/Retrovir
HIV Core Particle Immunostimulant	Rorer (Ft. Washington, PA)	seropositive HIV
IL-2 Interleukin-2	Cetus (Emerycille, CA)	AIDS, in combaintion w/Retrovir
IL-2 Interleukin-2	Hoffman-La Roche (Nutley, NJ)	AIDS, ARC, HIV, in combination w/Retrovir
Immune Globulin Intravenous (human)	Cutter Biological (Berkeley, CA)	pediatric AIDS, in combination w/Retrovir

Drug Name	Manufacturer	Indication
IMREG-1	Imreg (New Orleans, LA)	AIDS, Kaposi's sarcoma, ARC, PGL
IMREG-2	Imreg (New Orleans, LA)	AIDS, Kaposi's sarcoma, ARC, PGL
Imuthiol Diethyl Dithio Carbamate	Merieux Institute (Miami, FL)	AIDS, ARC
INTRON A Alpha-2 Interferon	Schering Plough (Madison, NJ)	Kaposi's sarcoma w/Retrovir: AIDS
Methionine-Enkephalin	TNI Pharmaceutical (Chicago, IL)	AIDS, ARC
MTP-PE Muramyl-Tripeptide	Ciba-Geigy Corp. (Summit, NJ)	Kaposi's sarcoma
Granulocyte Colony Stimulating Factor	Amgen (Thousand Oaks, CA)	AIDS, in combination w/Retrovir
rCD4 Recombinant Soluble Human CD4	Genentech (S. San Francisco, CA)	AIDS, ARC
Recombinant Soluble Human CD4	Biogen (Cambridge, MA)	AIDS, ARC

Drug Name	Manufacturer	Indication
Roferon-A Interferon Alfa 2a	Hoffman-La Roche (Nutley, NJ)	Kaposi's sarcoma AIDS, ARC, in combination w/Retrovir
SK&F106528 Soluble T4	Smith, Kline & French Laboratories (Philadelphia, PA)	HIV infection
Thymopentin	Immunobiology Research Institute (Annandale, NJ)	HIV infection
Tumor Necrosis Factor; TNF	Genentech (S. San Francisco, CA)	ARC, in combination w/gamma Interferon
	Anti-Infectives	
Clindamycin with Primaquine	Upjohn (Kalamazoo, MI)	PCP
Diflucan Fluconazole	Pfizer (New York, NY)	cryptococcal meningitis, candidiasis
Pastille Nystatin Pastille	Squibb Corp. (Princeton, NJ)	prevention of oral candidiasis
Ornidyl Eflornithine	Merrell Dow (Cincinnati, OH)	PCP

Drug Name	Manufacturer	Indication
Pentamidine Isethionate (IM & IV)	LyphoMed (Rosemont, IL)	PCP treatment
Piritrexim	Burroughs Wellcome (Rsch. Triangle Park, NC)	PCP treatment
Pentamidine isethionate for inhalation	Fisons Corporation (Bedford, MA)	PCP prophylaxis
Spiramycin	Phone-Poulenc Pharmaceuticals (Princeton, NJ)	cryptosporidial diarrhea
Intraconazole-R51211	Janssen Pharm. (Piscataway, NJ)	histoplasmosis; cryptococcal meningitis
Trimetrexate	Warner-Lambert	PCP
	Other	
Recombinant Human Erythropoietin	Ortho Pharm. Corp. (Raritan, NJ)	severe anemia assoc. and Retrovir therapy
Megestrol Acetate	Bristol-Myers (New York, NY)	treatment of anorexia assoc. w/AIDS

It will be understood that the scope of combinations of the antigenic conjugates of this invention with AIDS antivirals, immunomodulators, anti-infectives or vaccines is not limited to the list in the above Table, but includes in principle any combination with any pharmaceutical composition useful for the treatment of AIDS. The antigenic conjugates as AIDS or HIV vaccines of this invention include vaccines to be used pre- or post-exposure to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen.

The compound L-697,661 is 3-([4,7-dichloro-1,3-benzoxazol-2-yl)methyl]amino)-5-ethyl-6-methyl-pyridin-2(1H)-one or pharmaceutically acceptable salt thereof. The compound L-696,229 is 3-[2-(1,3-benzoxazol-2-yl)ethyl]-5-ethyl-6-methyl-pyridin-2(1H)-one or pharmaceutically acceptable salt thereof. The compound L-735,524 is N-(2(R)-hydroxy-1(S)-indanyl)-2(R)-phenylmethyl-4-(S)-hydroxy-5-(1-(4-(3-pyridyl-methyl)-2(S)-N'-(t-butylcarboxamido)-piperazinyl))-pentaneamide, or pharmaceutically acceptable salt thereof.

Biological Deposits

The cell line producing "447 antibody", also known as 447-52D, is a Human x Human x Mouse Heterohybridoma cell line, which was deposited on or before 12 April 1991 at the American Type Culture Collection, Rockville, Maryland, under the requirement of a U.S. Patent Deposit.

EXAMPLE 1

Library Construction

A. Random Library

A phage library containing random 15 amino acid epitopes was constructed by the methods of Scott, J.K. et al. Science 249, 386 (1990). In this protocol, synthetic 110 bp BglI fragments were prepared containing the degenerate coding sequence $(NNK)_{15}$, wherein N stands for an equal mixture of G, A, T and C, and K stands for an equal mixture of G and T. The library was constructed by ligating the synthetic 110 bp BglI fragments in phage fUSE5 and transfecting E. coli cells with the ligation product by electroporation.

The resulting phage oligopeptide epitope library (also known as Library ALPHA) had a complexity of approximately 40 x 10^6 different epitopes.

B. Semi Random Libraries

In order to determine the influence of sequence which flanks GPXR (SEQ. ID NO: 123) on binding and ultimately on the induction of a 447 like antibody response, and to determine the influence of potential loop formation, the following libraries were constructed in the same manner as Example 1A:

LIBRARY	Peptide Sequence	Complexity	SEQ. ID.
BETA	XXXXXXXXXGPXRXX	$92X10^6$	124
GAMMA	LLXXXXXGPXRXXXXXLL	$66X10^6$	125
DELTA	CXXXXXGPXRXXXXXC	$45X10^6$	126
EPSILON	CXXXXXXXXXXXXXXXC	$200X10^6$	127
	X is any amino acid		

Library BETA consists of random polypeptide sequences around GPXR (SEQ. ID NO: 123); library GAMMA adds terminal leucines for potential loop formation; library DELTA instead adds a terminal cysteine on each end for potential loop formation; library EPSILON is a control of any sequence with a cysteine loop.

EXAMPLE 2
Bead Coating Procedure

Polystyrene beads (d = 0.25 inch) were coated with between 1 and 10 µg of 447 antibody per ml in 50 mM $Na_2 CO_3$, pH 9.6, 0.02% sodium azide. (Note that any solid phase adsorbent should work). Beads were incubated in the antibody solution at 4°C overnight. The next day the coated beads were washed 3x with phosphate buffered saline and 1x with water. After washing, the antibody-coated beads were air dried and stored frozen at -20°C until needed. Before use, the antibody-coated beads were coated with 10 mg/ml BSA (to block free sites on the plastic) in TTBS (50 mM Tris pH 7.5, 150 mM NaCl, 0.5% (v/v) Tween 20) for 4 or more hours. Each batch

of beads was checked for antibody activity by its ability to bind ^{125}I protein A, before being used in a phage selection screen.

EXAMPLE 3

Stringent Phage Selection with Antibody-Coated Beads

A. First Method-Low Stringency

The random epitope phage library ALPHA was incubated at 4°C overnight with gentle rocking, with antibody-coated beads in TTBS, 1 mg/ml BSA. Typically, a total volume of 1cc containing about 10^{11} total phage was used. The next day the bead, containing bound phage, was washed 10 to 12 times in TTBS, in a volume of 10cc per wash, at room temperature, with a gentle rocking motion, for 10 minutes per wash. The liquid was carefully drained off the bead between each wash. After the last wash the bound phage were eluted off the bead by incubating for 5 minutes at room temperature in a minimal volume (typically 200 µl) of 0.1N HCl, adjusted to pH 2.2 with glycine, 1mg/ml BSA. The solution with the eluted phage was neutralized by adding 12 µl of 2M Tris, pH unadjusted, per 200 µl phage solution. The eluted phage were then used to infect E. coli K91K cells. Infected cells were plated onto LB agar plates containing 40 µg/ml tetracycline. Since the phage carry a tetracycline resistance marker, only infected cells grow on the plates. Typically, one bead selected between 5000 and 100,000 independent phage.

B. Second Method-High Stringency

The random epitope library or semi-random library was incubated at 4°C overnight with gentle rocking, with antibody-coated beads in TTBS, 1 mg/ml BSA. Typically, a total volume of 1cc containing on the order of 10^{11} total phage was used, corresponding to the complexity of the library x 1000. The next day the bead containing the bound phage was washed 10 times in TTBS, in a volume of 10cc per wash, at 65°C, with gentle rocking, for 10 minutes per wash. Note that 65°C in TTBS does not destroy phage. There followed one wash at room temperature in TTBS pH 4.0. The liquid was carefully drained off the bead between each wash. Next, the bound phage were eluted off the bead by incubating for 5 minutes at room temperature in 200 µl of 0.1N HCl, adjusted to pH 2.2 with glycine, 1 mg/ml BSA. The phage solution was neutralized by adding 12 µl of 2M Tris, pH unadjusted. The eluted phage were then used to infect E. coli K91K cells. Infected cells were grown in 1 x Luria broth containing 40 µg/ml tetracycline (250 cc) and incubated with shaking for 48 hours at 37°C. Phage were harvested and precipitated twice with PEG (polyethylene glycol). The precipitated phage were then titered and approximately 10^{10} of the first round selected phage were again incubated with a 447-antibody coated bead, washed as described above, regrown and harvested. Three cycles of selection and growth were performed. E. coli infected with phage were plated as clonal isolates.

EXAMPLE 4

Screening of Selected Phage with Antibody Lifts

After 1 or more rounds of selection according to Example 3, the infected E.coli colonies were screened for the ability to bind 447 antibody (using the same antibody as used to select the phage). This was done by growing the plates until the colonies reached a diameter of one to four mm, placing nitrocellulose disks onto the plates, lifting the disks and placing them in a solution of 10% evaporated milk, TTBS for 4 or more hours. After lifting, the plate containing the infected colonies were regrown for several hours at 37°C and placed at 4°C until needed. The nitrocellulose disks, at the end of 4 or more hours in the solution of 10% evaporated milk and TTBS, were washed 2-3x in TTBS and placed in TTBS and 1% milk and 0.5 to 1 µg/ml antibody solution. They were then incubated at 4°C overnight with gentle rocking. After incubation in the antibody solution, the disks were washed 4x in 100cc TTBS for 20 minutes with gentle rocking. They were then incubated in TTBS and 1% milk and I^{125} protein A (.5 to 1 µ curie/ml) for 1-1/2 to 3 hours. The disks were again washed 4x in 100 cc TTBS for 20 minutes. They were placed on X-ray film for 12 to 72 hours. The film was developed and colonies corresponding to dark spots were picked. If the plates were too dense to pick isolated colonies, the picked colony(ies) was replated at a lower density and the screen repeated to get clonal isolates.

EXAMPLE 5

PCR Sequencing

Phage infected E. coli K91K cells were grown overnight at 37°C in 1x Luria broth, 40 µg/ml tetracycline on a rollerdrum. The cells were pelleted and 1 µl of supernatant was used as the template in PCR reactions. The template was amplified using a 100-fold excess of one primer over the other. Template and oligonucleotide primers (Primer 1008: 5'-TCG AAA GCA AGC TGA TAA ACC G-3' SEQ ID NO:129, located 106 nucleotides upstream of random insert and Primer 1009: 5'-ACA GAC AGC CCT CAT AGT TAG CG-3' SEQ ID NO 130, located 87 nucleotides downstream from random insert) were reacted in a volume of 100 µl containing 50 mM KCl, 10 mM Tris-HCl pH 8.3, 1.5 mM $MgCl_2$, 0.01% (w/v) gelatin, 200 µM each dNTP, and 2.5 units Taq polymerase. Reactions were overlaid with mineral oil and amplified in a thermal cycler for an initial 8 minute 94°C incubation, then 30 cycles of 30 seconds at 94°C, 1 minute at 55°C and 2 minutes at 72°C followed by a 5 minute incubation at 72°C. The mineral oil was removed, 2 ml of water added to the reactions, and the sample centrifuged in a microconcentrator for 30 minutes at 1000 x g. The retentate volume was brought to 2 ml with water and centrifuged as above. The retentate was then collected by centrifugation for 2 minutes at 500 x g. Retentate concentrations were determined by electrophoresis on a 1% agarose gel containing 0.5 µg/ml Ethidium bromide and visualization under

ultraviolet light. The retentate was dried along with enough limiting primer from PCR reaction (or internal primer 1059-5'GTA AAT GAA TTT TCT GTA TGA GG 3' SEQ. ID NO:128 located 27 nucleotides downstream from insert) to give a 5:1 primer:template molar ratio. The DNA/primer mixture was resuspended in 8µl water and 2µl Tris•Buffer (200 mM Tris HCl, pH 7.5, 100 mM $MgCl_2$, 250 mM NaCl) Kit). The primer and template were annealed, and chain-termination sequencing reactions were set up. A 6% sequencing gel was run at 60 watts for approximately 1 hour and 30 minutes. The gel was dried and exposed to X-ray film overnight, and the sequence determined.

EXAMPLE 6

SPNE-pIII-$(His)_6$Fusions

The HIV/pIII fusion was expressed in E. Coli using the T7 polymerase system from Rosenberg, A.H. et. al., Gene 56, 125 (1987). The plasmid pET-3a (commercially available from Novagen, Madison, WI) was digested with Xba I and BamHI and the 5 kb vector fragment isolated. The isolated vector fragment was ligated with the Xba I,BgI II-digested HIV/pIII fusion prepared by polymerase chain reaction (PCR) of the candidate HIV fuse phage clones.

Two synthetic DNA oligomers were used to amplify a portion of the phage pIII gene (including the HIV sequences) and append sequences which permit

efficient expression and purification of the pIII product. The first synthetic DNA oligomers, 5' CCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGGCCGACG GGGCT 3' (Seq ID No: 131), has homology with the fuse phage pIII gene with sequences encoding the mature amino terminus of Ala-Asp-Gly-Ala. PCR amplification from this site incorporates sequences encoding the mature pIII protein, and rebuilds the pET-3a vector from the Xba I site to the initiating methionine.

The second synthetic DNA oligomer, sequence 5' CTCAGATCTATTAATGGTGATGGTGATGATGTATTTTGTCACAATCAA-TAGAAAATTC 3' (Seq ID No.: 132) encodes the reverse strand of the carboxyl-terminal portion of pIII ending with residues Cys-Asp-Lys-Ile (Seq ID No: 133). PCR with this oligo rebuilds the fuse phage pIII gene up to the transmembrane domain and appends six histidine residues to the carboxyl-terminal isoleucine. The presence of the histidine residues facilitates purification of the pIII fusion protein by metal chelation chromotography [Hochuli, E. et al., J. Chromat. 411, 177 (1987)] using nitrilotriacetic acid (NTA) resin (available from Qiagen, Chatsworth, CA).

Expression of the pIII fusion is obtained by transforming the expression plasmid into E. coli strain BL21 (DE3) [Rosenberg, A.H. et al., supra; U.S. Patent 4,952,496; Steen, et al., EMBO J 5, 1099 (1986).] This strain contains the T7 phage RNA polymerase gene under control of the lac operator/promoter. Addition of isopropylthiogalactoside (IPTG) at culture OD_{600}=0.6-0.8 induces T7 RNA polymerase expression

which transcribes pIII mRNA to high levels. This RNA is translated yielding pIII fusion protein which is harvested 3-4 hours post-induction and chromatographed on NTA resin.

EXAMPLE 7

Synthesis of Selected Oligopeptide

The oligopeptide LLRTIMIGPGRLLHS (SEQUENCE ID. NO. 23, hereinafter 473) was selected for immunological characterization. It was synthesized by the solid-phase method.

EXAMPLE 8

Extraction and Purification of OMPC

A. First Method

All materials, reagents and equipment were sterilized by filtration, steam autoclave or ethylene oxide, as appropriate; asceptic technique was used throughout.

A 300 gm (wet weight) aliquot of 0.5% phenol inactivated cell paste of Meningococcal group B11 was suspended in 1200 mls of distilled water then suspended by stirring magnetically for 20 minutes at room temperature. The suspended cells were pelleted at 20,000 xg for 45 minutes at 5°C.

For extraction, the washed cells were suspended in 1500 mls 0.1 M Tris, 0.01 M EDTA Buffer pH 8.5 with 0.5% sodium deoxycholate (TED Buffer) and homogenized with a 500 ml Sorvall omnimixer at

setting 3 for 60 seconds. The resulting suspension was transferred to ten Erlenmeyer flasks (500 ml) for extraction in a shaking water bath for 15 minutes at 56°C. The extract was centrifuged at 20,000 x g for 90 minutes at 5°C and the viscous supernatant fluid was decanted (volume = 1500 mls). The decanted fluid was very turbid and was recentrifuged to clarify further at 20,000 x g for 90 minutes at 5°C. The twice spun supernatant fluid was stored at 5°C. The extracted cell pellets were resuspended in 1500 mls TED Buffer. The suspension was extracted for 15 minutes at 56°C and recentrifuged at 20,000 x g for 90 minutes. The supernatant fluids which contained purified OMPC were decanted (volume = 1500 mls) and stored at 5°C.

B. Second Method

All material, reagents, equipment and filters were sterilized by heat, filtration or ethylene oxide. One exception was the K-2 ultracentrifuge which was sanitized with a 0.5% formalin solution. Laminar flow canopies provided sterility protection during equipment connections. Aseptic techniques were followed throughout the entire operations. Overnight storage of the protein was at 2-8°C between steps. A 0.2 micron sterile filtration was conducted just before the final diafiltration to ensure product sterility.

Two 600-liter batches of Neisseria meningitidis were fermented and killed with 0.5% phenol, then concentrated to roughly 25 liters using two 10 ft^2 0.2 micron polypropylene cross-flow

filtration membranes. The concentrated broth then was diafiltered with 125 liters of cell wash buffer (0.11 M Sodium Chloride, 17.6 mM Sodium Phosphate Diabasic, 23.3 mM Ammonium Chloride, 1.34 mM Potassium Chloride, adjusted to pH 7 with 85% Phosphoric Acid followed by 2.03 mM Magnesium Sulfate Heptahydrate).

For extraction, an equal volume of 2X-TED buffer (0.2M Tris, 0.02M EDTA adjusted to pH 8.5 with concentrated HCl followed by the addition of 1.0% sodium deoxycholate) was added to the cell slurry. The resulting slurry was heated to 56% 3°C and maintained at this temperature for 30 minutes to complete the extraction of OMPC from the cells.

For further purification, the extracted cell slurry was centrifuged at 30,000 x g (18,000 rpm) in a "one-pass" flow mode in a K-ultracentrifuge, and the supernatant stream was collected. The low-speed supernatant was concentrated to 10 liters on two 0.1-micron polysulfone autoclavable hollow-fiber membranes and collected in an 18 liter sterile bottle. The filtration equipment was given two 4-liter rinses with TED buffer (0.1M Tris, 0.01M EDTA, adjusted to pH 8.5 with concentrated HCl, followed by the addition of sodium deoxycholate to 0.5%) which was combined with the retentate. The retentate was subdivided into two or three equal parts. Each part was centrifuged at 80,000 x g (35,000 rpm) for 30 minutes. The OMPC protein was pelleted, and the majority of soluble proteins, nucleic acids and endotoxins remained in the supernatant. The supernatant was discarded. The

pelleted protein was resuspended by recirculating 55% 5°C TED buffer through the rotor. The first high-speed resuspensions were combined and subjected to a second low-speed spin. The second low-speed spin ensured that residual cell debris was removed from the product stream. The second low speed supernatant was subdivided into two or three equal parts. Each fraction was given two consecutive high-speed spins. All high-speed spins were operated under the same conditions and each further purified the OMPC protein.

For sterile filtration and final diafiltration, the third high-speed resuspensions were diluted with an equal volume of TED buffer and filtered through a 0.2 micron cellulose acetate filter. When all fractions were permeated, an 8 L TED buffer rinse was used to flush the filtration system. The permeate and rinse were combined and concentrated to 3 liters on a 0.1 micron polysulfone autoclavable hollow fiber membrane. The material then was diafiltered with 15 liters of sterile pyrogen free water. The retentate was collected in a 4-liter bottle along with a 1-L rinse to give the final product. The final aqueous suspension was stored at 2-8°C, as purified OMPC.

C. Third Method

OMPC is purified from 0.2 M LiCl-0.1M Na Acetate, pH 5.8, extracts by ultracentrifugation, by the method of C.E. Frasch et al. J. Exp. Med. 140, 87-104 (1974).

EXAMPLE 9

Oligopeptide 473 was conjugated to OMPC by the co-conjugation method of EP0467700 of Leanza, W.J. et al., to give 473-OMPC conjugate, as follows:

A. Thiolation of OMPC:

OMPC (43.4 mg, 10 mL) was pelleted by ultracentrifugation (43K rpm, 2h, 4°C). The pellet was resuspended in a sterile filtered (0.22µm) solution which consisted of: pH 11, 0.1 M borate buffer (4 mL), N-Acetyl homocysteine thiolactone (45 mg), DTT (15 mg), and EDTA (85 mg). The resulting solution was degassed and purged with nitrogen (process repeated 3x) and stored under N_2 overnight at room temperature (17 h). The thiolation mixture was transferred to a centrifuge tube and topped with pH 8.0, 0.1 M phosphate buffer (approximately 4.5 mL). The protein was pelleted via ultracentrifugation, resuspended (after homogenization) in pH 8.0, 0.1 M phosphate buffer, and repelleted by ultracentrifugation. This pellet was resuspended in 1X TED buffer, wtih a total resuspension volume of 7.0 mL. An Ellman's analysis on this solution (100 µL) revealed that it contained 0.961 µmol SH/mL solution (6.72 µmol SH total, 0.155 µmol SH/mg OMPC used).

B. Conjugation:

The beta-maleimidopropionyl peptide (5.8 µmol) was dissolved in acetonitrile (1.0 mL) giving Solution P. A solution of beta-maleimidopropionic

acid (5.5 μmol) in water (1.o mL) was prepared, which is Solution M.

Thiolated OMPC (6.0 mL, 5.77 μmol), which was prepared in step A, was transferred to a sterile 15 mL centrifuge tube. This solution was vortexed and solution M (420 μL, 2.31 μmol) added. The mixture was stirred briefly and allowed to age at room temperature (10 min). Next, the reaction mixture was vortexed and solution P (596 μL, 3.46 μmol) added. The reaction mixture was vortexed briefly and allowed to age at room temperature for 2 h.

The conjugate was spun in a clinical centrifuge to remove any precipitated material. The supernatant was removed and the conjugate was pelleted by ultracentrifugation (43K rpm, 2 h, 4°C). The pellet was resuspended in TED buffer (total volume 6.5 mL), affording 473-OMPC conjugate.

Lowry Protein Assay: 3.04 mg/mL

Amino Acid Analysis:

Lys: 835 nmol/mL

Beta-Ala: 157 nmol/mL

Nle: 175 nmol/mL

Loading (Based on Nle): 58 nmol peptide/mg OMPC

Loading % (w/w%; Based on Nle): 11%

EXAMPLE 10

Immunization Protocol for 473-OMPC conjugate

Four New Zealand white rabbits (2 to 2.5 kg) were immunized with the peptide 473-OMPC conjugate vaccine (the vaccine) in the following manner: For time zero inoculations the vaccine was formulated into complete Freund's adjuvant (CFA) [1:1(v/v) of CFA and 600µg/ml of conjugate in saline]. Each dose (1.0 ml) consisted of a total of 300 µg of vaccine. Each rabbit was inoculated with the vaccine preparation at two sites, by intra-muscular (im) injection, in the upper hind leg. Two booster inoculations were given to each rabbit at week 4 and week 8 post initial injection. The vaccine for these booster injections was formulated into incomplete Freund's adjuvant. Each dose also consisted of a total of 300 µg of vaccine.

Each rabbit was bled and sera was prepared by standard methods for anti-peptide ELISA tests (Example 10) and anti-HIV neutralization tests (Example 11). Sera collected represent time zero and biweekly intervals through week 14.

EXAMPLE 11

Measurement of Antibody Responses in Rabbits Immunized with 473-OMPC Conjugate Vaccine (ELISA).

Elicited anti-peptide antibody responses in vaccinated rabbits were determined by the use of an

enzyme-linked immunoadsorbent assay (ELISA). In this assay, microtiter plates were coated with about 0.5 µg peptide 473 per well using an overnight incubation of peptide solution at 36°C in a humidified atmosphere. Elicited anti-HIV isolate MN specific antibody responses were measured by the use of an anti-peptide 402 ELISA assay. In this assay the 402 peptide (primary sequence = NleCYNKRKRIHIGPGRAFYTTKNIIGC, SEQ. ID. NO. 122, with disulfide bonding between the two C residues) was the coating peptide. Peptide 402 is a cyclic representation of the HIV isolate MN gp120 V3 loop sequence.

For 473 ELISA tests, titers were determined with 0 time and weeks 2, 4, 6, 8, 10, 12 and 14 sera. See Table I. For 402 ELISA tests, titers were determined for weeks 10, 12 and 14 sera. See Table II, in which the ELISA antigen is 402 instead of 473. Test sera were diluted 5-fold serially, were reacted for 1 hr with the peptide adsorbed wells, and were washed extensively. Positive results were identified after reactions of phosphatase-conjugated goat anti-rabbit sera with each well for 1 hr at 36°C, washing and the addition of a solution of 1.0 mg/mL p-nitrophenyl phosphate (pNPP) in 10% diethanolamine, 0.5 mM $MgCl_2$ (pH 9.8) to each well. This last reaction proceeded for 30 minutes at room temperature and was stopped by addition of 3.0 N NaOH. Absorbance at 405 nm was determined by using a plate reader.

EXAMPLE 12

Measurement of Virus Neutralizing Antibody Responses Elicited in Rabbits Immunized with 473-OMPC Conjugates.

Neutralization of Infectivity in MT-4 Cells in vitro: For neutralization tests 2-fold serial dilutions of sera were made and 100 µL volumes were used in each test well in 96 well culture plates. All sera were heat inactivated before use. Generally 1:10 was the starting dilution of sera. An aliquot of 100 µL virus stock dilution was added to each test well. The HIV isolates used to determine virus neutralization by anti-473 rabbit sera were IIIB, MN, SF-2, AL-1 and WMJ-2. The virus-antisera mixtures were incubated at 37°C for 1 hr after which 1 x 10^4 MT-4 cells in 50 µL of culture medium were added to each well and the cultures were incubated for 7 days. The level of neutralization was determined by using the MTT dye reduction readout. MTT was added to each well to 500 µg/mL, incubated at 37°C for 2 hr, and solubilized after addition of acid-isopropanol (0.04N HCl in isopropanol) to approximately 50% of the volume of each well. A clearly distinguishable bluish-purple color develops in wells containing viable cells that are protected from infection due to virus neutralization by anti-473 antibody whereas wells containing MT-4 cells killed by the infection remain yellow. The neutralization endpoints were determined as the last dilution of antisera preparation that prevents cell killing. Uninfected

MT-4 cells were cultured with each test and a virus retitration was performed with each analysis.

For results, see Tables IIIA and IIIB. Table IIIA contains the neutralization data obtained in experiments using isolates MN, AL-1 (Alabama) and SF-2. Table IIIB contains that for WMJ-2 and 10 week only for isolate IIIB. Values given represent the reciprocal of the endpoint dilution.

TABLE I

Anti-473 peptide ELISA titers after vaccination with 473-OMPC.

		Anti-peptide ELISA titers							
		*		*	Weeks	*			
		0	2	4	6	8	10	12	14
	1	<20	<20	500	2,500	2,500	62,500	62,500	62,500
Rabbits	2	<20	<20	2,500	12,500	2,500	12,500	62,500	12,501
	3	<20	100	2,500	62,500	62,500	62,500	62,500	312,500
	4	<20	500	2,500	12,500	12,500	12,500	12,500	12,500

NOTE: Asterisks indicate the times of inoculation. All values are given as the reciprocal of the endpoint dilution.

TABLE II

Anti-402 peptide ELISA titers after vaccination with 473-OMPC.

		Anti-402 ELISA titers							
		*		*	Weeks	*			
		0	2	4	6	8	10	12	14
	1						100	20	20
Rabbits	2						500	50	100
	3						<100	<20	<20
	4						12,500	12,500	12,500

TABLE IIIA

In Vitro Neutralization by Anti 473-OMPC Sera.

MN Neutralization

		*			* Weeks	*		
		0	2	4	6	8	10	12
	1	<10			<10		<10	
Rabbits	2	<10			<10		<10	
	3	<10			<10		<10	
	4	<10			<10		<10	

Alabama Neutralization

		*			* Weeks	*		
		0	2	4	6	8	10	12
	1	<10			<10		<10	
Rabbits	2	<10			<10		<10	
	3	<10			<10		<10	
	4	<10			<10		20	

SF-2 Neutralization

		*			* Weeks	*		
		0	2	4	6	8	10	12
	1	<10			<10		80	
Rabbits	2	<10			160		160	
	3	<10			<10		<10	
	4	<10			<10		80	

TABLE IIIB

In Vitro Neutralization by Anti 473-OMPC Sera.

		WMJ-2 Neutralization						
		*		*	Weeks	*		
		0	2	4	6	8	10	12
Rabbits	1	<10			<10		<10	
	2	<10			<10		<10	
	3	<10			<10		<10	
	4	<10			<10		<10	

		IIIB Neutralization						
		*		*	Weeks	*		
		0	2	4	6	8	10	12
Rabbits	1	<10					<10	
	2	<10					<10	
	3	<10					<10	
	4	<10					<10	

While the foregoing specification teaches the principles of the present invention, with examples provided for the purpose of illustration, it will be understood that the practice of the invention encompasses all of the usual variations, adaptions, and modifications, as come within the scope of the claims and its equivalents.

SEQUENCE LISTING

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(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Pro Arg Leu Glu Thr His Phe Gly Pro Lys Arg Ser His Val Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Trp Arg Leu Gly Pro Gly Arg Gly Ser Met Pro Cys Arg Leu Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Gly Leu Leu Arg Val Leu Tyr Ala Phe Gly Pro Gly Arg Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Leu Val Trp Gln Arg Lys Val Phe Phe Gly Pro His Arg Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Ser Ser Ser Trp Ala Trp Arg His Leu Tyr Gly Pro Ala Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

His Ser Gln Ala Val Lys Phe Gly Pro Gly Arg Thr Leu Val Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Trp Asp Arg Gly Asn Ser Ser Gly Arg His Leu Gly Pro Ala Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Leu Gln Ala Arg Ser Lys Thr Tyr Phe Tyr Gly Pro Gly Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Trp His Leu Arg Val Arg Gly Ala His Phe Gly Pro Ala Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Trp Leu Arg Val Leu Leu Gly Pro Ala Arg Pro Ile Tyr Trp Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Leu Leu Gly Pro Ala Arg Ala Pro Val Arg Val Asn Leu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Lys Pro Arg Ala Pro Met Leu Phe Gly Pro Ala Arg Gly Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Leu Leu Ile Gly Pro Gly Arg Glu Leu Arg Pro Ile Asn Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Val Phe Lys Val Ile Asn Arg Ile Leu His Tyr Gly Pro Asn Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Phe Tyr Gly Pro Gly Arg Tyr Pro Pro Arg Phe Lys Leu Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asp Val Gly Trp Val Thr Gly Thr Gln His Tyr Gly Pro Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Leu Tyr Thr Cys Met Tyr Gly Pro Ser Arg His Ile Cys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Cys Ala Thr Ser Ile Gly Gly Val Leu Phe Gly Pro Gly Arg Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Arg Met Met Leu Gly Pro Gly Arg Asp Tyr Ala Gly Pro Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Thr Glu Leu Gly Arg Gly Tyr Ile Ser His Gly Pro Ala Arg Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Arg Ile Arg Leu Pro Arg Gly Pro Gly Arg Pro Gln Thr Thr Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

His Leu Gly Pro Ser Arg Gly Ala Asn Leu Gly Lys Ile Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Leu Arg Thr Ile Met Ile Gly Pro Gly Arg Leu Leu His Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu His Val Gly Pro Asn Arg Gly Lys Ser Glu Asp Asn Tyr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Gln Ile Ile Phe Ile Gly Pro Gly Arg Leu Gly Asn Gly Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Gln Leu Leu Ile Gly Pro Gly Arg Thr Val Gly Lys Ile Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Phe Tyr Thr Ser Gly Lys Thr Ile Phe Tyr Tyr Gly Pro Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Thr Lys Ile Gly Pro Gly Arg Val Phe Asp Gly Arg Trp Arg Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ala	Cys	Trp	Ser	Arg	Glu	Tyr	Gly	Pro	Ala	Arg	Met	Ser	Cys	Thr
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ile	Leu	Phe	Gly	Pro	Gly	Arg	Cys	Ser	Val	Asp	Ala	Val	Ser	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Tyr Leu Ala Met Arg Gly Ala Gly Tyr Met Ile Gly Pro Ala Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Cys Ser Val His Val Gly Ala Gly Arg Asn Ser Ala Trp Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asn Arg Tyr Gly Pro Gly Arg Val Gly Phe Val Arg Ser Gln Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala Arg Gly Trp Gly Gly Val Phe Tyr Gly Pro Gly Arg Gly Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Tyr Gly Arg Phe Ser Phe Gly Pro Gly Arg Gly Tyr Met Val Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Tyr Tyr Tyr Arg Asn Val Leu Val Gly Pro Gly Arg Trp Trp Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Trp Ser Trp Val Arg Leu Lys Ala Val Leu Leu Gly Pro Ser Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Phe Gln Glu Gly Gln Lys Val Leu Val Gly Pro Gly Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Cys Met Thr Ser Val Leu Val Gly Pro Gly Arg Gln Asp Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Ile Leu Arg Gln Pro Leu Leu Ile Gly Pro Gly Arg Ala Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp Asp Thr Leu Gly Trp Val Val Ser Asn Phe Gly Pro Gly Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Val Leu Arg Cys Phe Gly Pro Leu Arg Asp Ala Arg Cys Ser Val
1 5 10 15

35(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gln Ile Trp Tyr Phe Gly Pro Gly Arg Ser Gln Ser Gly Ser Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Met Val Val Gln Val Gly Pro Ala Arg Thr Phe Leu Gln Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Pro Ser Leu Phe Asn Ser Gly Val Arg Tyr Gly Pro Lys Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val His Phe Ile Gly Pro Gln Arg Gly Gly Asn Ser Ser His Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Tyr Ser Asp Leu Leu Leu Ser Lys Tyr Phe Gly Pro Gly Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Asp Gln Tyr Arg Val Leu Leu Trp Gly Pro Gly Arg Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val Leu Lys Ile Leu Arg His Ala Tyr Phe Gly Pro Gly Arg Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Val Arg His Met Gly Pro Gly Arg Gly Met Val Leu Gly Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Asn Tyr Phe Gly Pro Gly Arg Gly Gly Val Val Val Thr Gly His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Val Phe Gly Pro Gly Arg Thr Asn Pro Arg Ser Asn Leu Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Glu Arg Asp Leu Val Arg Phe Gly Pro Asn Arg Asp Trp Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asn Gly Leu Lys Leu Cys Arg Val Gly Pro Ser Arg Glu Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Phe Asp Gly Gln Ser Lys Val Val Leu Arg Gly Pro Gly Arg Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Val Lys Phe Gly Pro Gln Arg Ser Gly Gly Ala Thr Arg Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Random Epitope Library Alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile Thr Pro Arg Leu Tyr Gly Pro Ser Arg Met Arg Tyr Asn Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: consensus peptide for seq. Id Nos. 1-57.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Trp Asp Gly Leu Gly Trp Gln Ile Val His Phe Gly Pro Gly Arg Gly
1 5 10 15

Gly Asn Gly Ile Asn Leu Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Asn Lys Arg Glu Phe Gly Pro Ala Arg Ala Ala Arg Asn Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

His Arg Arg Asp Ile Gly Pro Ala Arg Thr Arg Glu Ile Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Ala Gly His Val Gly Pro Gly Arg Tyr Gly Ala Leu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser Ala Val His Leu Gly Pro Gln Arg Gln Arg Ala Thr Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Thr Arg His Leu Gly Pro Gly Arg Val Glu Gly Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Val His Arg Phe Gly Pro Gly Arg Gly Glu Gly Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Gly Tyr His Trp Gly Pro Gly Arg Gly Ser Val Glu Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gln Ala Trp His Phe Gly Pro Gly Arg Asp His Gly Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Ala Asn His Tyr Gly Pro Ser Arg Gly Pro Gly Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Leu Leu Gly Pro Gly Arg Gly Ser Ser Ser Val Arg Gly Glu Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ser Gly Trp Trp Gly Gly Val His Val Gly Pro Gly Arg Gly Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Trp Ser Lys Arg Glu Ser Val Met Phe Gly Pro Gly Arg Gly Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Trp Asp Ser Arg Ala Thr Leu Arg Leu Gly Pro Gly Arg Ser Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly Lys Val Phe Tyr Gly Pro Gly Arg Glu Trp His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Arg Val Phe Leu Gly Pro Gly Arg Gly Val Val Tyr Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Arg Val Gln Lys Leu Gly Pro Gly Arg Gln Thr Ala Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Leu Gly Pro Gly Arg Gly Gly Tyr Phe Gly Ala Gln Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Arg Lys Val Asn Ile Gly Pro Gly Arg Val His Gly Asn Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Arg Gly Val Lys Ile Gly Pro Gly Arg Ile Ala Ser Gly Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Lys Asp Leu His Ile Gly Pro Gly Arg Met Asp Gly Leu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala Gln Arg Ser His Leu Ile Gly Pro Gly Arg Ala Glu Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Lys Gln Val Arg Leu Gly Pro Ala Arg Gly Asp Ile Ile Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Arg Gln Val Met Leu Gly Pro Gly Arg Gly Asp Arg Leu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Arg Ser Val Leu Met Gly Pro Ala Arg Ser Thr Arg Val Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Lys Phe Val Glu Leu Gly Pro Gly Arg Lys Gly Gln Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Asp Arg Gly Ser Arg Phe Val Leu Leu Gly Pro Gly Arg Met Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Glu Gln Leu His Arg Leu Val Ala Phe Gly Pro Gly Arg Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu Pro Ser Val Asn Leu Gly Pro Gly Arg Asn Ala Arg Lys Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Gln His Arg Ala Ala Ser Val His Leu Gly Pro Ser Arg Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Leu Met Phe Val Arg Val Val Lys Leu Gly Pro Ala Arg Val Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Tyr Gly Leu Val Ile Arg Cys Glu Val Gly Pro Ser Arg Ser Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Arg Glu Leu His Met Gly Pro Gly Arg Ala Arg Pro Gly Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Cys Arg Val Asp Phe Gly Pro Gly Arg Leu Gly Ser Arg Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Asn Val Val Ala Ile Gly Pro Gly Arg Ser Asn Val Val Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Lys Glu Val His Phe Gly Pro Gly Arg Gly Gly Gln Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Xaa Xaa Tyr Leu Ile Gly Pro Gly Arg Gly Trp Glu Arg Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ala Gly Cys Gln Val Gly Pro Gly Arg Pro Xaa Cys Gly Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Arg Glu Val His Phe Gly Pro Arg Arg Asp Glu Pro Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ile Gly Arg Asn Leu Gly Pro Gly Arg Val Val Ser Asn Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Asn Val His Val Gly Pro Gly Arg Gly Gln Arg Thr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Arg Leu His Leu Val Gly Pro Ala Arg Val Ser Pro Leu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Ser Lys Val Glu Ile Gly Pro Gly Arg Gly Pro Leu Met Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ala Val Ile His Val Gly Pro Ser Arg Leu Lys Ser Gln Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Gly Arg Ile Asn Tyr Gly Pro Gly Ala Pro Gly Leu Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Glu Val His Tyr Tyr Gly Pro Gly Arg Arg Ala Pro Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Val Glu Arg His Leu Gly Pro Gly Arg Gly Leu Gln Met Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Asn Ser Phe His Leu Gly Pro Gly Arg Ser Arg Thr Tyr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Delta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Gly Val Val Lys Leu Gly Pro Gly Arg Thr Ala Gly Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Leu Ile Gly Pro Gly Arg Ser Ser Val Ala Met Thr Ile Arg Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Leu Val Arg Met Leu Gly Pro Gly Arg Gly Asn Asp Arg Thr His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gln Arg Gly Lys Thr Phe Tyr Gly Pro Gly Arg Gly Ser Gly Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Asp Arg Gly Lys Ile Val Tyr Gly Pro Gly Arg Thr Gln Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Epsilon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Asp Trp Arg Ser Val His Ile Gly Pro Ala Arg Arg Glu Val Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Gly Phe Ser Ser Ser Arg Val Leu Val Gly Pro Gly Arg Gly Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Val Lys Arg Arg Asp Ala Val His Ala Gly Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Asp Ser Glu Arg Val Gly Val Leu Leu Gly Pro Gly Arg Gly Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Leu Gly Arg Pro Ala Val Arg Phe Gly Pro Gly Arg Ile Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Ser Arg Phe Arg Glu Trp His Val Gly Pro Gly Arg Val Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Ala Leu Arg Lys Val Arg Xaa Tyr Gly Pro Ala Arg Gln Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ile Gly Val Thr Arg Ala Leu Phe Phe Gly Pro Gly Arg Gly Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Ser Leu Ser Arg Ala His Val His Arg Gly Pro Gly Arg Val Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Leu Val Tyr Arg Ala Ala His Tyr Gly Pro Gly Arg Gly Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Semi Random Epitope Library Beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Arg Gly Trp Arg Pro Val Leu Ala Val Gly Pro Gly Arg Trp Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Nle Cys Tyr Asn Lys Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala
1 5 10 15

Phe Tyr Thr Thr Lys Asn Ile Ile Gly Cys
20 25

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Internal Consensus Peptide.
Compare with SEQ ID. NO. 146.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gly Pro Xaa Arg
1

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Library BETA formula

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Arg Xaa Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Library GAMMA formula

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Leu Leu Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Arg Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Leu Leu

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Library DELTA formula

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Cys Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Arg Xaa Xaa Xaa Xaa Xaa Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Library EPSILON formula

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Cys

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA primer

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTAAATGAAT TTTCTGTATG AGG 23

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA primer

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TCGAAAGCAA GCTGATAAAC CG 22

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA primer

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACAGACAGCC CTCATAGTTA GCG 23

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA primer

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CCCTCTAGAA ATAATTTTGT TTAACTTTAA GAAGGAGATA TACATATGGC CGACGGGGCT 60

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA primer

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CTCAGATCTA TTAATGGTGA TGGTGATGAT GTATTTTGTC ACAATCAATA GAAAATTC 58

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: carboxy terminal fragment of pIII
internal to fusion peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Cys Asp Lys Ile
1 4

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of SEQ Id Nos. 59-89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys Arg Ser Val His Leu Gly Pro Gly Arg Gly Asp Gly Leu Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of SEQ ID Nos. 59-89 without Cys constraints.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Arg Ser Val His Leu Gly Pro Gly Arg Gly Asp Gly Leu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of library BETA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Asp Gly Ser Arg Arg Ala Val His Leu Gly Pro Gly Arg Gly Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of library GAMMA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Leu Leu Lys Glu Val His Phe Gly Pro Gly Arg Gly Arg Gly Gly Arg
1 5 10 15

Leu Leu

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of library DELTA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Cys Arg Gly Val His Leu Gly Pro Gly Arg Gly Ala Arg Met Ser Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of library EPSILON

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Cys Asp Arg Gly Ser Val Leu Ile Gly Pro Gly Arg Gly Ser Ser Xaa
1 5 10 15

Gly Cys

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of SEQ ID Nos: 90-121 without Cys constraints.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Asp Leu Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Ser Pro
1 5 10 15

Arg Ser

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANIT-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of SEQ ID NOS: 90-121 with Cys constraints

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Cys Asp Leu Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Ser
1 5 10 15

Pro Arg Ser Cys
20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of SEQ ID NOS: 59-121 without Cys constraints

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asp Ser Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Glu Gly
1 5 10 15

Leu Ser

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Consensus peptide of SEQ ID NOS: 59-121 with Cys constraints.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Cys Asp Ser Ser Arg Arg Val Val His Leu Gly Pro Gly Arg Gly Glu
1 5 10 15

Gly Leu Ser Cys
20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(VI) IMMEDIATE SOURCE: Modified consensus peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Trp Arg Ser Val His Leu Gly Pro Gly Arg Gly Ser Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Modified consensus peptide with Cys constraints

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Cys Trp Arg Ser Val His Leu Gly Pro Gly Arg Gly Ser Gly Ser Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE: Selected internal consensus peptide, wherein Xaa is any amino acid except Gly. Compare with Seq. ID No. 123.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Pro Xaa Arg

WHAT IS CLAIMED IS:

1. An antigenic conjugate of HIV-specific, selected principal neutralization epitopes covalently linked to purified outer membrane proteosome of Neisseria, wherein said conjugate is of the formula

$$(SPNE)_n\text{-}(OMPC)$$

wherein:

SPNE	is the selected principal neutralization epitope of HIV, which is a polypeptide of one or more amino acid sequences of Table A or fragment thereof, said fragment having at least 5 amino acids in length and including the GPXR loop region or homolog thereof;
n	indicates the number of polypeptides of SPNE covalently linked to OMPC and is 1-50;
-	indicates covalent linkage;
OMPC	is purified outer membrane proteosome of Neisseria,

said conjugate optionally substituted with a^-, which is an anion or polyanion at physiological pH, said a^- consisting of one to five residues of anions selected from the group consisting of carboxylic, sulfonic, proprionic or phosphonic acid,

or pharmaceutically acceptable salt thereof.

2. The antigenic conjugate of Claim 1 wherein the conjugate is a covalent conjugate of OMPC of Neisseria and the epitope is any of the consensus peptide sequences 58, 134-145.

3. The antigenic conjugate of Claim 1 wherein the conjugate is a covalent conjugate of OMPC of Neisseria and a polypeptide epitope of 5 or more amino acids of any of the consensus peptide sequences 58, 134-145.

4. The antigenic conjugate of Claim 1 wherein the covalent linkage between SPNE and OMPC consists essentially of a bigeneric spacer.

5. The antigenic conjugate of Claims 1-4, wherein said OMPC is derived from Neisseria meningitidis.

6. An AIDS vaccine comprising an antigenic conjugate of HIV-specific selected principal neutralization epitopes having one or more of the sequences of Table A, said epitopes covalently linked to purified outer membrane proteosome of Neisseria, said conjugate mixed with a suitable immunological adjuvant, carrier or vector, said vaccine to be used pre- and post-exposure to prevent or treat HIV infection or disease, said vaccine capable of eliciting specific HIV neutralizing antibodies, said purified outer membrane proteosome optionally substituted with a^-, which is an anion or polyanion at physiological pH, said a^- consisting of one to

five residues of anions selected from the group consisting of carboxylic, sulfonic, proprionic or phosphonic acid.

7. An AIDS vaccine of Claim 6 wherein the conjugate is a covalent conjugate of OMPC of Neisseria and the epitope is any of the consensus peptide sequences 58, 134-145.

8. An AIDS vaccine of Claim 6 wherein the conjugate is a covalent conjugate of OMPC of Neisseria and a polypeptide epitope of 5 or more amino acids of any of the consensus peptide sequences of Table A.

9. An AIDS vaccine of Claim 6 wherein the covalent linkage between SPNE and OMPC consists essentially of a bigeneric spacer.

10. An AIDS vaccine of Claim 6 wherein said OMPC is derived from Neisseria meningitidis.

11. A pharmaceutical composition comprising an antigenic conjugate of HIV-specific selected principal neutralization epitopes having one or more of the sequences of Table A, said epitopes covalently linked to purified outer membrane proteosome of Neisseria, said conjugate mixed with a suitable immunological adjuvant, said composition useful as a vaccine capable of producing specific HIV neutralizing antibody in mammals, said purified outer membrane proteosome optionally substituted with a^-, which is

an anion or polyanion at physiological pH, said a^- consisting of one to five residues of anions selected from the group consisting of carboxylic, sulfonic, proprionic or phosphonic acid.

12. The pharmaceutical composition of Claim 11 wherein the conjugate is a covalent conjugate of OMPC of Neisseria and the epitope is any of the consensus peptide sequences 58, 134-145.

13. The pharmaceutical composition of Claim 11 wherein the conjugate is a covalent conjugate of OMPC of Neisseria and a polypeptide epitope of 5 or more amino acids with any of the consensus peptide sequences 58, 134-145.

14. The pharmaceutical composition of Claim 11 wherein the covalent linkage between SPNE and OMPC consists essentially of a bigeneric spacer.

15. The pharmaceutical composition of Claim 11 wherein said OMPC is derived from Neisseria meningitidis.

16. A method of vaccinating against ARC or AIDS, comprising administering an effective amount of a pharmaceutical composition comprising an antigenic conjugate of HIV-specific selected principal neutralization epitopes having one or more of the sequences of Table A, said epitopes covalently linked to purified outer membrane proteosome of Neisseria, said conjugate mixed with a suitable immunological

adjuvant, said purified outer membrane proteosome optionally substituted with a^-, which is an anion or polyanion at physiological pH, said a^- consisting of one to five residues of anions selected from the group consisting of carboxylic, sulfonic, proprionic or phosphonic acid.

17. A method of preventing infection by HIV, comprising administering an effective amount of a pharmaceutical composition comprising an antigenic conjugate of HIV-specific selected principal neutralization epitopes having one or more sequences of Table A, said epitopes covalently linked to purified outer membrane proteosome of Neisseria, said conjugate mixed with a suitable immunological adjuvant, said purified outer membrane proteosome optionally substituted with a^-, which is an anion or polyanion at physiological pH, said a^- consisting of one to five residues of anions selected from the group consisting of carboxylic, sulfonic, proprionic or phosphonic acid.

18. A method of treating AIDS, comprising administering an effective amount of a pharmaceutical composition comprising an antigenic conjugate of HIV-specific selected principal neutralization epitopes having one or more sequences of Table A, said epitopes covalently linked to purified outer membrane proteosome of Neisseria, said conjugate mixed with a suitable immunological adjuvant, said purified outer membrane proteosome optionally substituted with a^-, which is an anion or polyanion

at physiological pH, said a^- consisting of one to five residues of anions selected from the group consisting of carboxylic, sulfonic, proprionic or phosphonic acid.

19. A method of treating infection by HIV, comprising administering an effective amount of a pharmaceutical composition comprising an antigenic conjugate of HIV-specific selected principal neutralization epitopes having one or more sequences of Table A, said epitopes covalently linked to purified outer membrane proteosome of Neisseria, said conjugate mixed with a suitable immunological adjuvant, said purified outer membrane proteosome optionally substituted with a^-, which is an anion or polyanion at physiological pH, said a^- consisting of one to five residues of anions selected from the group consisting of carboxylic, sulfonic, or propionic phosphonic acid.

20. HIV-specific selected principal neutralization epitope polypeptides having any of sequences 1-121, 134-145.

21. HIV-specific selected principal neutralization consensus polypeptide having any of the sequences 58, 134-145.

22. A method of screening phage epitope libraries with a screening antibody, comprising the steps of

(a) subjecting a phage epitope library to one or more cycles of low or high stringency selection, yielding selected phage, and

(b) identifying the selected phage with antibody lifts.

23. A method of screening phage epitope libraries with a screening antibody, comprising the steps of

(a) subjecting a phage epitope library to one or more cycles of high stringency selection, yielding selected phage, and

(b) identifying the selected phage with antibody lifts.

24. A method of screening phage epitope libraries with a screening antibody, comprising the steps of

(a) contacting a solid-phase supported screening antibody with a sample of phage epitope library in excess of library complexity;

(b) washing the product of step(a) to remove unbound and/or low affinity phage within a temperature range of between about room temperature to about 65°C, and retaining the complex of solid-phase supported screening antibody bound to phage;

(c) eluting the bound phage of said complex of step (b) with buffer having pH between about 1.0 and about 2.3;

(d) neutralizing the solution containing eluted phage, yielding selected phage.

25. The method of Claim 24, wherein step (b) is the high stringency procedure, comprising

1. washing the product of step (a) 3 to 20 times in buffer at about neutral pH at about 65°C, to effect removal of unbound phage; and

2. washing the fraction of step 1 containing solid-phase supported screening antibody bound to phage, by about a 2-5 minute contact in a buffer having a pH between about 3.0 and about 5.0 at a temperature between about 4°C and about 37°C, to effect removal of low affinity phage epitopes, to give the complex of solid-phase supported screening antibody bound to phage.

26. The method of Claim 24, wherein step (b) is the low stringency wash procedure.

27. A method of selecting phage epitope libraries with a screening antibody by high stringency selection procedure, comprising the steps of

(a) contacting a solid-phase supported screening antibody with a sample of phage epitope library in excess of library complexity;

(b1) washing the product of step (a) 3 to 20 times in buffer at about neutral pH at about 65°C, to effect removal of unbound phage;

(b2) washing the fraction of step (b1) containing solid-phase supported screening antibody bound to phage, by about a 2-5 minute contact in a buffer having a pH between about 3.0 and about 5.0 at a temperature between about 4°C and about 37°C, to

effect removal of low affinity phage epitopes from the complex of solid-phase supported screening antibody bound to phage;

(c) eluting the bound phage off said complex by incubating between about 1 to about 15 minutes in a buffer of pH between about 1.0 and about 2.3, containing between about 0.1 to 10 µg/ml of a blocking agent, without detergent, at a temperature between about 37°C and about 40°C; and

(d) neutralizing the solution containing the eluted phage, yielding phage selected by the high stringency procedure.

28. The method of Claim 27, comprising the high stringency selection procedure and identification with antibody lifts, comprising the additional steps of

(e) plating out cells infected with phage selected by the high stringency procedure of step (d) and growing up the resulting colonies, yielding mature plates;

(f) overlaying the mature plates with a disk or other surface that binds protein, and immediately removing said overlaid disk;

(g) blocking the overlaid disk by incubating the disk for at least 2 hours, in a buffer of a pH between about 5.0 and about 8.0, containing about 0.1% (v/v) to about 1% (v/v) neutral detergent, in about 1% to about 20% blocking agent, within a temperature range of about 4°C to about 80°C, yielding blocked disks;

(h) washing the blocked disks to remove excess blocking agent by incubating the disk for at least 10 minutes in a buffer of a pH between about 5.0 and about 8.0, containing about 0.1%(v/v) to about 1% (v/v) neutral detergent, within the temperature range of about 4°C to about 80°C, yielding washed blocked disks;

(i) contacting the resulting disk with screening antibody by incubating the disks for at least 4 hours, in a buffer containing between about 0.1 to about 5 µg/ml screening antibody, in a temperature range between about 4°C and about 65°C;

(j) washing the disk to effect removal of unbound antibody;

(k) labeling the bound antibody with a labeled second-stage reagent; and

(l) identifying colonies corresponding to bound antibody.

SEQUENCE 58 AND IMPORTANT VARIANTS

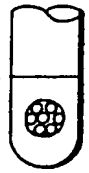
Seq.58:	Trp	Asp	Gly	Lys	Gly	Trp	Gln	Ile	Val	His
	1	Tyr	Ala	Met	5	Asn				10
				Gly		Tyr				
Seq.58,con't:	Phe	Gly	Pro	Gly	Arg	Gly	Gly	Asn	Gly	Ile
					15					20
Seq.58,con't:	Asn	Leu	Gly	Ala						

FIG.1

FIG.2

FLOW CHART OF SAMPLE SCREENING

RANDOM EPITOPE PHAGE LIBRARY, COMPLEXITY OF 30 x 10^6 DIFFERENT EPITOPES, PHAGE CARRY TETRACYCLINE RESISTANT MARKER

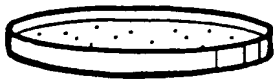


BEAD COATED WITH TARGET ANTIBODY

INCUBATE APPROXIMATELY 10^{11} PHAGE WITH BEAD OVERNIGHT,

WASH 10 x TO REMOVE NONSPECIFIC BINDING PHAGE,

INFECT E. coli, PLATE ON TETRACYCLINE PLATES



TYPICALLY,GET 30,000 TO 100,000 SELECTED COLONIES EACH INFECTED WITH A DIFFERENT PHAGE

LIFT COLONIES ONTO NITROCELLULOSE DISKS, SAVE AGAR PLATES

PROBE DISKS WITH ORIGINAL SCREENING ANTIBODY

PICK POSITIVES, REPLATE AT LOW DENSITY TO GET CLONAL E. coli COLONIES EXPRESSING PHAGE

SEQUENCE GENE IN PHAGE ENCODING SELECTED EPITOPE

USE IDENTIFIED EPITOPE AS VACCINE (COUPLED TO IMMUNOENHANCER OR FUSED TO VIRAL PROTEIN, FOR EXAMPLE, TO N-TERMINUS OF HBsAg PROTEIN)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/06751

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :C12P 21/06; C12N 7/04;
US CL :435/69.1; 235.1; 935/79

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1; 235.1; 935/79

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, Dialog, search terms: epitope library, screening, phage library, peptides, antibodies

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Proceedings National Academy of Sciences, volume 87, issued August 1990, Cwirla et al, "Peptides On Phage: A Vast Library of Peptides for Identifying Ligands", pages 6378-6382, see entire article.	22-28
X Y	Science, Volume 249, issued 27 July 1990, Scott et al, "Searching for Peptide Ligands With An Epitope Library", pages 386-390, see entire article.	22-23 24-28
Y	Proceedings National Academy of Sciences, Volume 80, issued March 1983, Young et al, "Efficient Isolation of Genes by Using Antibody Probes", pages 1194-1198, especially 1196-1197.	22-28

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be part of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 27 September 1993	Date of mailing of the international search report 05 OCT 1993
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. NOT APPLICABLE	Authorized officer CHRISTINE M. NUCKER Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/06751

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Proceedings National Academy of Sciences, Volume 89, issued March 1992, Cull et al, "Screening for Receptor Ligands Using Large Libraries of Peptides linked To The C Terminus of The lac Repressor", pages 1865-1869, see entire article.	22-28

INTERNATIONAL SEARCH REPORT

In. national application No.
PCT/US93/06751

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
(Telephone Practice)
Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Claims 22-28.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

1. Claims 22-28, drawn to a first method of screening for peptides, classified in classes 435 and 935, subclasses 69.1, 235.1 and 79.

2. Claims 1-22, drawn to a conjugate, vaccine, pharmaceutical composition and second method of preventing or treating infection by using the peptides, classified in classes 424 and 530, subclasses 89 and 350, 395.

The claims of the two groups are directed to different inventions which are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept. The inventions are not linked in methods and steps and perform completely different functions. Note PCT Rule 13 and 37 CFR 1.475.